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(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
1 November 2001 (01.11.2001)

PCT

(10) International Publication Number
WO 01/81555 A2

(51) International Patent Classification⁷: C12N 9/00

(21) International Application Number: PCT/US01/12992

(22) International Filing Date: 20 April 2001 (20.04.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/199,021	20 April 2000 (20.04.2000)	US
60/200,226	28 April 2000 (28.04.2000)	US
60/202,339	5 May 2000 (05.05.2000)	US
60/203,505	11 May 2000 (11.05.2000)	US
60/205,564	18 May 2000 (18.05.2000)	US
60/207,739	26 May 2000 (26.05.2000)	US
60/208,795	1 June 2000 (01.06.2000)	US

(63) Related by continuation (CON) or continuation-in-part (CIP) to earlier applications:

US	60/200,226 (CIP)
Filed on	28 April 2000 (28.04.2000)
US	60/199,021 (CIP)
Filed on	20 April 2000 (20.04.2000)
US	60/202,339 (CIP)
Filed on	5 May 2000 (05.05.2000)
US	60/203,505 (CIP)
Filed on	11 May 2000 (11.05.2000)
US	60/205,564 (CIP)
Filed on	18 May 2000 (18.05.2000)
US	60/207,739 (CIP)
Filed on	26 May 2000 (26.05.2000)
US	60/208,795 (CIP)
Filed on	1 June 2000 (01.06.2000)

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,

[Continued on next page]

(54) Title: HUMAN KINASES

(57) Abstract: The invention provides human kinases (PKIN) and polynucleotides which identify and encode PKIN. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of PKIN.

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LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

- (84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

HUMAN KINASES

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human kinases and to the
5 use of these sequences in the diagnosis, treatment, and prevention of cancer, immune disorders,
disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the
assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid
sequences of human kinases.

10 BACKGROUND OF THE INVENTION

Kinases comprise the largest known enzyme superfamily and vary widely in their target
molecules. Kinases catalyze the transfer of high energy phosphate groups from a phosphate donor to
a phosphate acceptor. Nucleotides usually serve as the phosphate donor in these reactions, with most
kinases utilizing adenosine triphosphate (ATP). The phosphate acceptor can be any of a variety of
15 molecules, including nucleosides, nucleotides, lipids, carbohydrates, and proteins. Proteins are
phosphorylated on hydroxyamino acids. Addition of a phosphate group alters the local charge on the
acceptor molecule, causing internal conformational changes and potentially influencing
intermolecular contacts. Reversible protein phosphorylation is the primary method for regulating
protein activity in eukaryotic cells. In general, proteins are activated by phosphorylation in response
20 to extracellular signals such as hormones, neurotransmitters, and growth and differentiation factors.
The activated proteins initiate the cell's intracellular response by way of intracellular signaling
pathways and second messenger molecules such as cyclic nucleotides, calcium-calmodulin, inositol,
and various mitogens, that regulate protein phosphorylation.

Kinases are involved in all aspects of a cell's function, from basic metabolic processes, such
25 as glycolysis, to cell-cycle regulation, differentiation, and communication with the extracellular
environment through signal transduction cascades. Inappropriate phosphorylation of proteins in cells
has been linked to changes in cell cycle progression and cell differentiation. Changes in the cell cycle
have been linked to induction of apoptosis or cancer. Changes in cell differentiation have been linked
to diseases and disorders of the reproductive system, immune system, and skeletal muscle.

30 There are two classes of protein kinases. One class, protein tyrosine kinases (PTKs),
phosphorylates tyrosine residues, and the other class, protein serine/threonine kinases (STKs),
phosphorylates serine and threonine residues. Some PTKs and STKs possess structural
characteristics of both families and have dual specificity for both tyrosine and serine/threonine
residues. Almost all kinases contain a conserved 250-300 amino acid catalytic domain containing
35 specific residues and sequence motifs characteristic of the kinase family. The protein kinase catalytic

domain can be further divided into 11 subdomains. N-terminal subdomains I-IV fold into a two-lobed structure which binds and orients the ATP donor molecule, and subdomain V spans the two lobes. C-terminal subdomains VI-XI bind the protein substrate and transfer the gamma phosphate from ATP to the hydroxyl group of a tyrosine, serine, or threonine residue. Each of the 11 subdomains contains

5 specific catalytic residues or amino acid motifs characteristic of that subdomain. For example, subdomain I contains an 8-amino acid glycine-rich ATP binding consensus motif, subdomain II contains a critical lysine residue required for maximal catalytic activity, and subdomains VI through IX comprise the highly conserved catalytic core. PTKs and STKs also contain distinct sequence motifs in subdomains VI and VIII which may confer hydroxyamino acid specificity.

10 In addition, kinases may also be classified by additional amino acid sequences, generally between 5 and 100 residues, which either flank or occur within the kinase domain. These additional amino acid sequences regulate kinase activity and determine substrate specificity. (Reviewed in Hardie, G. and S. Hanks (1995) The Protein Kinase Facts Book, Vol I, pp. 17-20 Academic Press, San Diego CA.). In particular, two protein kinase signature sequences have been identified in the

15 kinase domain, the first containing an active site lysine residue involved in ATP binding, and the second containing an aspartate residue important for catalytic activity. If a protein analyzed includes the two protein kinase signatures, the probability of that protein being a protein kinase is close to 100% (PROSITE: PDOC00100, November 1995).

Protein Tyrosine Kinases

20 Protein tyrosine kinases (PTKs) may be classified as either transmembrane, receptor PTKs or nontransmembrane, nonreceptor PTK proteins. Transmembrane tyrosine kinases function as receptors for most growth factors. Growth factors bind to the receptor tyrosine kinase (RTK), which causes the receptor to phosphorylate itself (autophosphorylation) and specific intracellular second messenger proteins. Growth factors (GF) that associate with receptor PTKs include epidermal GF,

25 platelet-derived GF, fibroblast GF, hepatocyte GF, insulin and insulin-like GFs, nerve GF, vascular endothelial GF, and macrophage colony stimulating factor.

Nontransmembrane, nonreceptor PTKs lack transmembrane regions and, instead, form signaling complexes with the cytosolic domains of plasma membrane receptors. Receptors that function through non-receptor PTKs include those for cytokines and hormones (growth hormone and

30 prolactin), and antigen-specific receptors on T and B lymphocytes.

Many PTKs were first identified as oncogene products in cancer cells in which PTK activation was no longer subject to normal cellular controls. In fact, about one third of the known oncogenes encode PTKs. Furthermore, cellular transformation (oncogenesis) is often accompanied by increased tyrosine phosphorylation activity (Charbonneau, H. and N.K. Tonks (1992) *Annu. Rev. Cell Biol.* 8:463-493). Regulation of PTK activity may therefore be an important strategy in

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controlling some types of cancer.

Protein Serine/Threonine Kinases

Protein serine/threonine kinases (STKs) are nontransmembrane proteins. A subclass of STKs are known as ERKs (extracellular signal regulated kinases) or MAPs (mitogen-activated protein
5 kinases) and are activated after cell stimulation by a variety of hormones and growth factors. Cell stimulation induces a signaling cascade leading to phosphorylation of MEK (MAP/ERK kinase) which, in turn, activates ERK via serine and threonine phosphorylation. A varied number of proteins represent the downstream effectors for the active ERK and implicate it in the control of cell proliferation and differentiation, as well as regulation of the cytoskeleton. Activation of ERK is
10 normally transient, and cells possess dual specificity phosphatases that are responsible for its down-regulation. Also, numerous studies have shown that elevated ERK activity is associated with some cancers. Other STKs include the second messenger dependent protein kinases such as the cyclic-AMP dependent protein kinases (PKA), calcium-calmodulin (CaM) dependent protein kinases, and the mitogen-activated protein kinases (MAP); the cyclin-dependent protein kinases; checkpoint
15 and cell cycle kinases; Numb-associated kinase (Nak); human Fused (hFu); proliferation-related kinases; 5'-AMP-activated protein kinases; and kinases involved in apoptosis.

The second messenger dependent protein kinases primarily mediate the effects of second messengers such as cyclic AMP (cAMP), cyclic GMP, inositol triphosphate, phosphatidylinositol, 3,4,5-triphosphate, cyclic ADP ribose, arachidonic acid, diacylglycerol and calcium-calmodulin. The
20 PKAs are involved in mediating hormone-induced cellular responses and are activated by cAMP produced within the cell in response to hormone stimulation. cAMP is an intracellular mediator of hormone action in all animal cells that have been studied. Hormone-induced cellular responses include thyroid hormone secretion, cortisol secretion, progesterone secretion, glycogen breakdown, bone resorption, and regulation of heart rate and force of heart muscle contraction. PKA is found in
25 all animal cells and is thought to account for the effects of cAMP in most of these cells. Altered PKA expression is implicated in a variety of disorders and diseases including cancer, thyroid disorders, diabetes, atherosclerosis, and cardiovascular disease (Isselbacher, K.J. et al. (1994) Harrison's Principles of Internal Medicine, McGraw-Hill, New York NY, pp. 416-431, 1887).

The casein kinase I (CKI) gene family is another subfamily of serine/threonine protein
30 kinases. This continuously expanding group of kinases have been implicated in the regulation of numerous cytoplasmic and nuclear processes, including cell metabolism, and DNA replication and repair. CKI enzymes are present in the membranes, nucleus, cytoplasm and cytoskeleton of eukaryotic cells, and on the mitotic spindles of mammalian cells (Fish, K.J. et al. (1995) *J. Biol. Chem.* 270:14875-14883).

35 The CKI family members all have a short amino-terminal domain of 9-76 amino acids, a

highly conserved kinase domain of 284 amino acids, and a variable carboxyl-terminal domain that ranges from 24 to over 200 amino acids in length (Cegielska, A. et al. (1998) J. Biol. Chem. 273:1357-1364). The CKI family is comprised of highly related proteins, as seen by the identification of isoforms of casein kinase I from a variety of sources. There are at least five mammalian isoforms, α , β , γ , δ , and ϵ . Fish et al., identified CKI-epsilon from a human placenta cDNA library. It is a basic protein of 416 amino acids and is closest to CKI-delta. Through recombinant expression, it was determined to phosphorylate known CKI substrates and was inhibited by the CKI-specific inhibitor CKI-7. The human gene for CKI-epsilon was able to rescue yeast with a slow-growth phenotype caused by deletion of the yeast CKI locus, HRR250 (Fish et al., supra).

10 The mammalian circadian mutation tau was found to be a semidominant autosomal allele of CKI-epsilon that markedly shortens period length of circadian rhythms in Syrian hamsters. The tau locus is encoded by casein kinase I-epsilon, which is also a homolog of the *Drosophila* circadian gene double-time. Studies of both the wildtype and tau mutant CKI-epsilon enzyme indicated that the mutant enzyme has a noticeable reduction in the maximum velocity and autophosphorylation state. 15 Further, *in vitro*, CKI-epsilon is able to interact with mammalian PERIOD proteins, while the mutant enzyme is deficient in its ability to phosphorylate PERIOD. Lowrey et al., have proposed that CKI-epsilon plays a major role in delaying the negative feedback signal within the transcription-translation-based autoregulatory loop that composes the core of the circadian mechanism. Therefore the CKI-epsilon enzyme is an ideal target for pharmaceutical compounds influencing circadian 20 rhythms, jet-lag and sleep, in addition to other physiologic and metabolic processes under circadian regulation (Lowrey, P.L. et al. (2000) Science 288:483-491).

Homeodomain-interacting protein kinases (HIPKs) are serine/threonine kinases and novel members of the DYRK kinase subfamily (Hofmann, T.G. et al., (2000) Biochimie 82:1123-7). HIPKs contain a conserved protein kinase domain separated from a domain that interacts with 25 homeoproteins. HIPKs are nuclear kinases, and HIPK2 is highly expressed in neuronal tissue (Kim, Y.H. et al., (1998) J. Biol. Chem. 273:25875-9; Wang, Y. et al., (2001) Biochim. Biophys. Acta 1518:168-172). HIPKs act as corepressors for homeodomain transcription factors. This corepressor activity is seen in posttranslational modifications such as ubiquitination and phosphorylation, each are important in the regulation of cellular protein function (Kim, Y.H. et al., (1999) Proc. Nat. Acad. 30 Sci. U.S.A. 96:12350-5).

Calcium-Calmodulin Dependent Protein Kinases

Calcium-calmodulin dependent (CaM) kinases are involved in regulation of smooth muscle contraction, glycogen breakdown (phosphorylase kinase), and neurotransmission (CaM kinase I and CaM kinase II). CaM dependent protein kinases are activated by calmodulin, an intracellular calcium 35 receptor, in response to the concentration of free calcium in the cell. Many CaM kinases are also

activated by phosphorylation. Some CaM kinases are also activated by autophosphorylation or by other regulatory kinases. CaM kinase I phosphorylates a variety of substrates including the neurotransmitter-related proteins synapsin I and II, the gene transcription regulator, CREB, and the cystic fibrosis conductance regulator protein, CFTR (Haribabu, B. et al. (1995) EMBO J. 14:3679-3686). CaM kinase II also phosphorylates synapsin at different sites and controls the synthesis of catecholamines in the brain through phosphorylation and activation of tyrosine hydroxylase. CaM kinase II controls the synthesis of catecholamines and serotonin, through phosphorylation/activation of tyrosine hydroxylase and tryptophan hydroxylase, respectively (Fujisawa, H. (1990) BioEssays 12:27-29). The mRNA encoding a calmodulin-binding protein kinase-like protein was found to be enriched in mammalian forebrain. This protein is associated with vesicles in both axons and dendrites and accumulates largely postnatally. The amino acid sequence of this protein is similar to CaM-dependent STKs, and the protein binds calmodulin in the presence of calcium (Godbout, M. et al. (1994) J. Neurosci. 14:1-13).

Mitogen-Activated Protein Kinases

The mitogen-activated protein kinases (MAP) which mediate signal transduction from the cell surface to the nucleus via phosphorylation cascades are another STK family that regulates intracellular signaling pathways. Several subgroups have been identified, and each manifests different substrate specificities and responds to distinct extracellular stimuli (Egan, S.E. and R.A. Weinberg (1993) Nature 365:781-783). MAP kinase signaling pathways are present in mammalian cells as well as in yeast. The extracellular stimuli which activate MAP kinase pathways include epidermal growth factor (EGF), ultraviolet light, hyperosmolar medium, heat shock, endotoxic lipopolysaccharide (LPS), and pro-inflammatory cytokines such as tumor necrosis factor (TNF) and interleukin-1 (IL-1). Altered MAP kinase expression is implicated in a variety of disease conditions including cancer, inflammation, immune disorders, and disorders affecting growth and development.

Cyclin-Dependent Protein Kinases

The cyclin-dependent protein kinases (CDKs) are STKs that control the progression of cells through the cell cycle. The entry and exit of a cell from mitosis are regulated by the synthesis and destruction of a family of activating proteins called cyclins. Cyclins are small regulatory proteins that bind to and activate CDKs, which then phosphorylate and activate selected proteins involved in the mitotic process. CDKs are unique in that they require multiple inputs to become activated. In addition to cyclin binding, CDK activation requires the phosphorylation of a specific threonine residue and the dephosphorylation of a specific tyrosine residue on the CDK.

Another family of STKs associated with the cell cycle are the NIMA (never in mitosis)-related kinases (Neks). Both CDKs and Neks are involved in duplication, maturation, and separation of the microtubule organizing center, the centrosome, in animal cells (Fry, A.M. et al. (1998) EMBO

J. 17:470-481).

Checkpoint and Cell Cycle Kinases

In the process of cell division, the order and timing of cell cycle transitions are under control of cell cycle checkpoints, which ensure that critical events such as DNA replication and chromosome segregation are carried out with precision. If DNA is damaged, e.g. by radiation, a checkpoint pathway is activated that arrests the cell cycle to provide time for repair. If the damage is extensive, apoptosis is induced. In the absence of such checkpoints, the damaged DNA is inherited by aberrant cells which may cause proliferative disorders such as cancer. Protein kinases play an important role in this process. For example, a specific kinase, checkpoint kinase 1 (Chk1), has been identified in yeast and mammals, and is activated by DNA damage in yeast. Activation of Chk1 leads to the arrest of the cell at the G2/M transition (Sanchez, Y. et al. (1997) Science 277:1497-1501). Specifically, Chk1 phosphorylates the cell division cycle phosphatase CDC25, inhibiting its normal function which is to dephosphorylate and activate the cyclin-dependent kinase Cdc2. Cdc2 activation controls the entry of cells into mitosis (Peng, C.-Y. et al. (1997) Science 277:1501-1505). Thus, activation of Chk1 prevents the damaged cell from entering mitosis. A similar deficiency in a checkpoint kinase, such as Chk1, may also contribute to cancer by failure to arrest cells with damaged DNA at other checkpoints such as G2/M.

Proliferation-Related Kinases

Proliferation-related kinase is a serum/cytokine inducible STK that is involved in regulation of the cell cycle and cell proliferation in human megakaryocytic cells (Li, B. et al. (1996) J. Biol. Chem. 271:19402-19408). Proliferation-related kinase is related to the polo (derived from *Drosophila* polo gene) family of STKs implicated in cell division. Proliferation-related kinase is downregulated in lung tumor tissue and may be a proto-oncogene whose deregulated expression in normal tissue leads to oncogenic transformation.

5'-AMP-activated protein kinase

A ligand-activated STK protein kinase is 5'-AMP-activated protein kinase (AMPK) (Gao, G. et al. (1996) J. Biol. Chem. 271:8675-8681). Mammalian AMPK is a regulator of fatty acid and sterol synthesis through phosphorylation of the enzymes acetyl-CoA carboxylase and hydroxymethylglutaryl-CoA reductase and mediates responses of these pathways to cellular stresses such as heat shock and depletion of glucose and ATP. AMPK is a heterotrimeric complex comprised of a catalytic alpha subunit and two non-catalytic beta and gamma subunits that are believed to regulate the activity of the alpha subunit. Subunits of AMPK have a much wider distribution in non-lipogenic tissues such as brain, heart, spleen, and lung than expected. This distribution suggests that its role may extend beyond regulation of lipid metabolism alone.

Kinases in Apoptosis

Apoptosis is a highly regulated signaling pathway leading to cell death that plays a crucial role in tissue development and homeostasis. Deregulation of this process is associated with the pathogenesis of a number of diseases including autoimmune disease, neurodegenerative disorders, and cancer. Various STKs play key roles in this process. ZIP kinase is an STK containing a C-terminal leucine zipper domain in addition to its N-terminal protein kinase domain. This C-terminal domain appears to mediate homodimerization and activation of the kinase as well as interactions with transcription factors such as activating transcription factor, ATF4, a member of the cyclic-AMP responsive element binding protein (ATF/CREB) family of transcriptional factors (Sanjo, H. et al. (1998) *J. Biol. Chem.* 273:29066-29071). DRAK1 and DRAK2 are STKs that share homology with the death-associated protein kinases (DAP kinases), known to function in interferon- γ induced apoptosis (Sanjo et al., *supra*). Like ZIP kinase, DAP kinases contain a C-terminal protein-protein interaction domain, in the form of ankyrin repeats, in addition to the N-terminal kinase domain. ZIP, DAP, and DRAK kinases induce morphological changes associated with apoptosis when transfected into NIH3T3 cells (Sanjo et al., *supra*). However, deletion of either the N-terminal kinase catalytic domain or the C-terminal domain of these proteins abolishes apoptosis activity, indicating that in addition to the kinase activity, activity in the C-terminal domain is also necessary for apoptosis, possibly as an interacting domain with a regulator or a specific substrate.

RICK is another STK recently identified as mediating a specific apoptotic pathway involving the death receptor, CD95 (Inohara, N. et al. (1998) *J. Biol. Chem.* 273:12296-12300). CD95 is a member of the tumor necrosis factor receptor superfamily and plays a critical role in the regulation and homeostasis of the immune system (Nagata, S. (1997) *Cell* 88:355-365). The CD95 receptor signaling pathway involves recruitment of various intracellular molecules to a receptor complex following ligand binding. This process includes recruitment of the cysteine protease caspase-8 which, in turn, activates a caspase cascade leading to cell death. RICK is composed of an N-terminal kinase catalytic domain and a C-terminal "caspase-recruitment" domain that interacts with caspase-like domains, indicating that RICK plays a role in the recruitment of caspase-8. This interpretation is supported by the fact that the expression of RICK in human 293T cells promotes activation of caspase-8 and potentiates the induction of apoptosis by various proteins involved in the CD95 apoptosis pathway (Inohara et al., *supra*).

Mitochondrial Protein Kinases

A novel class of eukaryotic kinases, related by sequence to prokaryotic histidine protein kinases, are the mitochondrial protein kinases (MPKs) which seem to have no sequence similarity with other eukaryotic protein kinases. These protein kinases are located exclusively in the mitochondrial matrix space and may have evolved from genes originally present in respiration-dependent bacteria which were endocytosed by primitive eukaryotic cells. MPKs are responsible for

phosphorylation and inactivation of the branched-chain alpha-ketoacid dehydrogenase and pyruvate dehydrogenase complexes (Harris, R.A. et al. (1995) *Adv. Enzyme Regul.* 34:147-162). Five MPKs have been identified. Four members correspond to pyruvate dehydrogenase kinase isozymes, regulating the activity of the pyruvate dehydrogenase complex, which is an important regulatory enzyme at the interface between glycolysis and the citric acid cycle. The fifth member corresponds to a branched-chain alpha-ketoacid dehydrogenase kinase, important in the regulation of the pathway for the disposal of branched-chain amino acids. (Harris, R.A. et al. (1997) *Adv. Enzyme Regul.* 37:271-293). Both starvation and the diabetic state are known to result in a great increase in the activity of the pyruvate dehydrogenase kinase in the liver, heart and muscle of the rat. This increase contributes in both disease states to the phosphorylation and inactivation of the pyruvate dehydrogenase complex and conservation of pyruvate and lactate for gluconeogenesis (Harris (1995) *supra*).

KINASES WITH NON-PROTEIN SUBSTRATES

15 Lipid and Inositol kinases

Lipid kinases phosphorylate hydroxyl residues on lipid head groups. A family of kinases involved in phosphorylation of phosphatidylinositol (PI) has been described, each member phosphorylating a specific carbon on the inositol ring (Leevers, S.J. et al. (1999) *Curr. Opin. Cell. Biol.* 11:219-225). The phosphorylation of phosphatidylinositol is involved in activation of the protein kinase C signaling pathway. The inositol phospholipids (phosphoinositides) intracellular signaling pathway begins with binding of a signaling molecule to a G-protein linked receptor in the plasma membrane. This leads to the phosphorylation of phosphatidylinositol (PI) residues on the inner side of the plasma membrane by inositol kinases, thus converting PI residues to the biphosphate state (PIP₂). PIP₂ is then cleaved into inositol triphosphate (IP₃) and diacylglycerol. These two products act as mediators for separate signaling pathways. Cellular responses that are mediated by these pathways are glycogen breakdown in the liver in response to vasopressin, smooth muscle contraction in response to acetylcholine, and thrombin-induced platelet aggregation.

PI 3-kinase (PI3K), which phosphorylates the D3 position of PI and its derivatives, has a central role in growth factor signal cascades involved in cell growth, differentiation, and metabolism. PI3K is a heterodimer consisting of an adapter subunit and a catalytic subunit. The adapter subunit acts as a scaffolding protein, interacting with specific tyrosine-phosphorylated proteins, lipid moieties, and other cytosolic factors. When the adapter subunit binds tyrosine phosphorylated targets, such as the insulin responsive substrate (IRS)-1, the catalytic subunit is activated and converts PI (4,5) biphosphate (PIP₂) to PI (3,4,5) P₃ (PIP₃). PIP₃ then activates a number of other proteins, including PKA, protein kinase B (PKB), protein kinase C (PKC), glycogen synthase kinase (GSK)-3,

and p70 ribosomal s6 kinase. PI3K also interacts directly with the cytoskeletal organizing proteins, Rac, rho, and cdc42 (Shepherd, P.R. et al. (1998) Biochem. J. 333:471-490). Animal models for diabetes, such as *obese* and *fat* mice, have altered PI3K adapter subunit levels. Specific mutations in the adapter subunit have also been found in an insulin-resistant Danish population, suggesting a role
5 for PI3K in type-2 diabetes (Shepard, supra).

An example of lipid kinase phosphorylation activity is the phosphorylation of D-erythro-sphingosine to the sphingolipid metabolite, sphingosine-1-phosphate (SPP). SPP has emerged as a novel lipid second-messenger with both extracellular and intracellular actions (Kohama, T. et al. (1998) J. Biol. Chem. 273:23722-23728). Extracellularly, SPP is a ligand for the G-protein
10 coupled receptor EDG-1 (endothelial-derived, G-protein coupled receptor). Intracellularly, SPP regulates cell growth, survival, motility, and cytoskeletal changes. SPP levels are regulated by sphingosine kinases that specifically phosphorylate D-erythro-sphingosine to SPP. The importance of sphingosine kinase in cell signaling is indicated by the fact that various stimuli, including platelet-derived growth factor (PDGF), nerve growth factor, and activation of protein kinase C,
15 increase cellular levels of SPP by activation of sphingosine kinase, and the fact that competitive inhibitors of the enzyme selectively inhibit cell proliferation induced by PDGF (Kohama et al., supra).

Purine Nucleotide Kinases

The purine nucleotide kinases, adenylate kinase (ATP:AMP phosphotransferase, or AdK) and
20 guanylate kinase (ATP:GMP phosphotransferase, or GuK) play a key role in nucleotide metabolism and are crucial to the synthesis and regulation of cellular levels of ATP and GTP, respectively. These two molecules are precursors in DNA and RNA synthesis in growing cells and provide the primary source of biochemical energy in cells (ATP), and signal transduction pathways (GTP). Inhibition of various steps in the synthesis of these two molecules has been the basis of many antiproliferative
25 drugs for cancer and antiviral therapy (Pillwein, K. et al. (1990) Cancer Res. 50:1576-1579).

AdK is found in almost all cell types and is especially abundant in cells having high rates of ATP synthesis and utilization such as skeletal muscle. In these cells AdK is physically associated with mitochondria and myofibrils, the subcellular structures that are involved in energy production and utilization, respectively. Recent studies have demonstrated a major function for AdK in
30 transferring high energy phosphoryls from metabolic processes generating ATP to cellular components consuming ATP (Zelevnikar, R.J. et al. (1995) J. Biol. Chem. 270:7311-7319). Thus AdK may have a pivotal role in maintaining energy production in cells, particularly those having a high rate of growth or metabolism such as cancer cells, and may provide a target for suppression of its activity to treat certain cancers. Alternatively, reduced AdK activity may be a source of various
35 metabolic, muscle-energy disorders that can result in cardiac or respiratory failure and may be

treatable by increasing AdK activity.

GuK, in addition to providing a key step in the synthesis of GTP for RNA and DNA synthesis, also fulfills an essential function in signal transduction pathways of cells through the regulation of GDP and GTP. Specifically, GTP binding to membrane associated G proteins mediates the activation of cell receptors, subsequent intracellular activation of adenylyl cyclase, and production of the second messenger, cyclic AMP. GDP binding to G proteins inhibits these processes. GDP and GTP levels also control the activity of certain oncogenic proteins such as p21^{ras} known to be involved in control of cell proliferation and oncogenesis (Bos, J.L. (1989) Cancer Res. 49:4682-4689). High ratios of GTP:GDP caused by suppression of GuK cause activation of p21^{ras} and promote oncogenesis. Increasing GuK activity to increase levels of GDP and reduce the GTP:GDP ratio may provide a therapeutic strategy to reverse oncogenesis.

GuK is an important enzyme in the phosphorylation and activation of certain antiviral drugs useful in the treatment of herpes virus infections. These drugs include the guanine homologs acyclovir and bucciclovir (Miller, W.H. and R.L. Miller (1980) J. Biol. Chem. 255:7204-7207; Stenberg, K. et al. (1986) J. Biol. Chem. 261:2134-2139). Increasing GuK activity in infected cells may provide a therapeutic strategy for augmenting the effectiveness of these drugs and possibly for reducing the necessary dosages of the drugs.

Pyrimidine Kinases

The pyrimidine kinases are deoxycytidine kinase and thymidine kinase 1 and 2. Deoxycytidine kinase is located in the nucleus, and thymidine kinase 1 and 2 are found in the cytosol (Johansson, M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11941-11945). Phosphorylation of deoxyribonucleosides by pyrimidine kinases provides an alternative pathway for *de novo* synthesis of DNA precursors. The role of pyrimidine kinases, like purine kinases, in phosphorylation is critical to the activation of several chemotherapeutically important nucleoside analogues (Arner E.S. and S. Eriksson (1995) Pharmacol. Ther. 67:155-186).

The discovery of new human kinases and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of human kinases.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, human kinases, referred to collectively as "PKIN" and individually as "PKIN-1," "PKIN-2," "PKIN-3," "PKIN-4," "PKIN-5," "PKIN-6," "PKIN-7," "PKIN-8," "PKIN-9," "PKIN-10," "PKIN-11," "PKIN-12," "PKIN-13," "PKIN-14,"

“PKIN-15,” “PKIN-16,” “PKIN-17,” and “PKIN-18.” In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-18.

10 The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence
15 selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-18. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:19-36.

20 Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a
25 biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

30 The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group
35 consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino

acid sequence selected from the group consisting of SEQ ID NO:1-18. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

5 Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an
10 amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18.

 The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of
15 SEQ ID NO:19-36, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

20 Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of
25 SEQ ID NO:19-36, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a
30 hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

 The invention further provides a method for detecting a target polynucleotide in a sample,
35 said target polynucleotide having a sequence of a polynucleotide selected from the group consisting

of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as

an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional PKIN, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. The method comprises a) combining the polypeptide with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of

the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:19-36, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, ii) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, ii) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the present invention.

Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of the polypeptides.

Table 4 lists the cDNA and genomic DNA fragments which were used to assemble
5 polynucleotide sequences of the invention, along with selected fragments of the polynucleotide sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

10 Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

15 Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

20 It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

25 Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing
30 the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"PKIN" refers to the amino acid sequences of substantially purified PKIN obtained from any
35 species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and

human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of PKIN. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of PKIN either by directly interacting with
5 PKIN or by acting on components of the biological pathway in which PKIN participates.

An "allelic variant" is an alternative form of the gene encoding PKIN. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to
10 allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding PKIN include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as PKIN or a
15 polypeptide with at least one functional characteristic of PKIN. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding PKIN, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding PKIN. The encoded protein may also be "altered," and may contain deletions, insertions, or
20 substitutions of amino acid residues which produce a silent change and result in a functionally equivalent PKIN. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of PKIN is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged
25 amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic
30 molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence.
35 Amplification is generally carried out using polymerase chain reaction (PCR) technologies well

known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of PKIN. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of PKIN either by
5 directly interacting with PKIN or by acting on components of the biological pathway in which PKIN participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind PKIN polypeptides can be prepared using intact polypeptides or using fragments
10 containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen
15 used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified
25 sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or
30 translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic PKIN, or of any oligopeptide thereof,
35 to induce a specific immune response in appropriate animals or cells and to bind with specific

antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

5 A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding PKIN or fragments of PKIN may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be
10 associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been
15 assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

20 "Conservative amino acid substitutions" are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

25	Original Residue	Conservative Substitution
	Ala	Gly, Ser
	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
30	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
35	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr

5	Ser Thr Trp Tyr Val	Cys, Thr Ser, Val Phe, Tyr His, Phe, Trp Ile, Leu, Thr
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Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

A "fragment" is a unique portion of PKIN or the polynucleotide encoding PKIN which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:19-36 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:19-36, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:19-36 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish
5 SEQ ID NO:19-36 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:19-36 and the region of SEQ ID NO:19-36 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-18 is encoded by a fragment of SEQ ID NO:19-36. A fragment of SEQ ID NO:1-18 comprises a region of unique amino acid sequence that specifically identifies
10 SEQ ID NO:1-18. For example, a fragment of SEQ ID NO:1-18 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-18. The precise length of a fragment of SEQ ID NO:1-18 and the region of SEQ ID NO:1-18 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

15 A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

20 The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

25 Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS
30 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms
35 is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment

Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the

site of substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 3

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term "humanized antibody" refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized

after the "washing" step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill
5 in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature
10 under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al.
15 (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC
20 concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions
25 will be readily apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A
30 hybridization complex may be formed in solution (e.g., C_0t or R_0t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" and "addition" refer to changes in an amino acid or nucleotide
35 sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

5 An "immunogenic fragment" is a polypeptide or oligopeptide fragment of PKIN which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of PKIN which is useful in any of the antibody production methods disclosed herein or known in the art.

10 The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of PKIN. For example, modulation
15 may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of PKIN.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the
20 antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where
25 necessary to join two protein coding regions, in the same reading frame.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript
30 elongation, and may be pegylated to extend their lifespan in the cell.

"Post-translational modification" of an PKIN may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of PKIN.

35 "Probe" refers to nucleic acid sequences encoding PKIN, their complements, or fragments

thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes.

"Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping

Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, *supra*. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

"Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing PKIN, nucleic acids encoding PKIN, or fragments thereof may comprise a bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or

cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular
5 structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are
10 removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

15 "Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular cell
20 type or tissue under given conditions at a given time.

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based
25 on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

30 A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with
35 a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in

vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection,

- 5 transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of
10 the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an
15 "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to
20 another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a
25 propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at
30 least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

- 35 The invention is based on the discovery of new human kinases (PKIN), the polynucleotides

encoding PKIN, and the use of these compositions for the diagnosis, treatment, or prevention of cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are human kinases. For example, SEQ ID NO:12 is 95% identical to a human adenylate kinase (GenBank ID g28577) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2). The BLAST probability score is $2.4e-112$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. Data from BLIMPS, MOTIFS, and PROFILE analysis; from BLAST analysis using the DOMO and PRODOM databases; and from HMMER analysis using the PFAM database further support the categorization of SEQ ID NO:12 as an adenylate kinase. (See Table 3). In an alternative example,

SEQ ID NO:13 is 92% identical to rat PCTAIRE 3 (GenBank ID g2257588) as determined by the Basic Local Alignment Search Tool (BLAST). The BLAST probability score is $1.4e-210$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance (Table 2). PCTAIRE 1, 2, and 3 comprise a subfamily of Cdc2-related kinases that are primarily expressed in post-mitotic cells. PCTAIRE 2 and PCTAIRE 3 are expressed in the brain (Hirose, T. *et al.*, (1997) Eur. J. Biochem. 249:481-488; Okuda, T. *et al.*, (1992) Oncogene 7:2249-2258). SEQ ID NO:13 also contains a kinase active site domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:13 is a kinase. In another alternative example, SEQ ID NO:18 is 86% identical to human cell cycle related kinase (GenBank ID g4090958) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $9.2e-85$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:18 also contains a eukaryotic protein kinase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) Data from BLIMPS, MOTIFS, and PROFILESCAN analyses provide further corroborative evidence that SEQ ID NO:18 is a cell cycle related kinase. SEQ ID NO:1-11 and SEQ ID NO:14-17 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-18 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:19-36 or that distinguish between SEQ ID NO:19-36 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 6311370H1 is the

identification number of an Incyte cDNA sequence, and NERDTDN03 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 70518523D1). Alternatively, the identification numbers in 5 may refer to GenBank cDNAs or ESTs (e.g., g1860144) which contributed to the assembly of the full length polynucleotide sequences. Alternatively, the identification numbers in column 5 may refer to coding regions predicted by Genscan analysis of genomic DNA. For example, GNN.g5924006_004.edit is the identification number of a Genscan-predicted coding sequence, with g5924006 being the GenBank identification number of the sequence to which Genscan was applied. The Genscan-predicted coding sequences may have been edited prior to assembly. (See Example IV.)

10 Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. (See Example V.) Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon-stretching" algorithm. (See Example V.) In some cases, Incyte cDNA coverage redundant with the sequence coverage shown in column 5 was

15 obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which

20 were used to assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

The invention also encompasses PKIN variants. A preferred PKIN variant is one which has at least about 80%, or alternatively at least about 90%, or alternatively at least about 95%, or even at least about 98% amino acid sequence identity to the PKIN amino acid sequence, and which contains

25 at least one functional or structural characteristic of PKIN.

The invention also encompasses polynucleotides which encode PKIN. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:19-36, which encodes PKIN. The polynucleotide sequences of SEQ ID NO:19-36, as presented in the Sequence Listing, embrace the equivalent RNA sequences,

30 wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding PKIN. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or alternatively at least about 95%, or even at least about 98% polynucleotide

35 sequence identity to the polynucleotide sequence encoding PKIN. A particular aspect of the

invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:19-36 which has at least about 70%, or alternatively at least about 85%, or alternatively at least about 95%, or even at least about 98% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:19-36. Any one of the
5 polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of PKIN.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding PKIN, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be
10 produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring PKIN, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode PKIN and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring PKIN under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding PKIN or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide
20 occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding PKIN and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode PKIN and PKIN derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding PKIN or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:19-36 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in
35 "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding PKIN may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.)

Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence
5 into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the
10 emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

15 In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode PKIN may be cloned in recombinant DNA molecules that direct expression of PKIN, or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express PKIN.

20 The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter PKIN-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-
25 mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat.
30 Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of PKIN, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired
35 properties. These preferred variants may then be pooled and further subjected to recursive rounds of

DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of
5 homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding PKIN may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) *Nucleic Acids Symp. Ser. 7*:215-223; and Horn, T. et al. (1980) *Nucleic Acids Symp. Ser. 7*:225-232.)
10 Alternatively, PKIN itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) *Science* 269:202-204.) Automated synthesis
15 may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of PKIN, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid
20 chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active PKIN, the nucleotide sequences encoding PKIN or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains
25 the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding PKIN. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding PKIN. Such signals
30 include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding PKIN and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be
35 provided by the vector. Exogenous translational elements and initiation codons may be of various

origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression
5 vectors containing sequences encoding PKIN and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

10 A variety of expression vector/host systems may be utilized to contain and express sequences encoding PKIN. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus);
15 plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Engelhard, E.K. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945; Takamatsu, N. (1987) *EMBO J.* 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New
20 York NY, pp. 191-196; Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659; and Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) *Cancer Gen. Ther.* 5(6):350-356; Yu, M. et al. (1993) *Proc. Natl. Acad. Sci.*
25 *USA* 90(13):6340-6344; Buller, R.M. et al. (1985) *Nature* 317(6040):813-815; McGregor, D.P. et al. (1994) *Mol. Immunol.* 31(3):219-226; and Verma, I.M. and N. Somia (1997) *Nature* 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding PKIN. For example, routine cloning,
30 subcloning, and propagation of polynucleotide sequences encoding PKIN can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPT1 plasmid (Life Technologies). Ligation of sequences encoding PKIN into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for
35 in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of

nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of PKIN are needed, e.g. for the production of antibodies, vectors which direct high level expression of PKIN may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

5 Yeast expression systems may be used for production of PKIN. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel,
10 1995, supra; Bitter, G.A. et al. (1987) Methods Enzymol. 153:516-544; and Scorer, C.A. et al. (1994) Bio/Technology 12:181-184.)

Plant systems may also be used for expression of PKIN. Transcription of sequences encoding PKIN may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J.
15 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology
20 (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding PKIN may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain
25 infective virus which expresses PKIN in host cells. (See, e.g., Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of
30 DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression
35 of PKIN in cell lines is preferred. For example, sequences encoding PKIN can be transformed into

cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk*⁻ and *apr*⁻ cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding PKIN is inserted within a marker gene sequence, transformed cells containing sequences encoding PKIN can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding PKIN under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding PKIN and that express PKIN may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of PKIN using either

specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PKIN is preferred, but a
5 competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

10 A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding PKIN include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding PKIN, or any fragments thereof, may be cloned into a vector
15 for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for
20 ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding PKIN may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence
25 and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode PKIN may be designed to contain signal sequences which direct secretion of PKIN through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of
30 the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the
35 American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct

modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding PKIN may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric PKIN protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of PKIN activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the PKIN encoding sequence and the heterologous protein sequence, so that PKIN may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled PKIN may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ³⁵S-methionine.

PKIN of the present invention or fragments thereof may be used to screen for compounds that specifically bind to PKIN. At least one and up to a plurality of test compounds may be screened for specific binding to PKIN. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of PKIN, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which PKIN binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express PKIN, either as a secreted

protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing PKIN or cell membrane fractions which contain PKIN are then contacted with a test compound and binding, stimulation, or inhibition of activity of either PKIN or the compound is analyzed.

- 5 An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with PKIN, either in solution or affixed to a solid support, and detecting the binding of PKIN to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a
- 10 labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a solid support.

- PKIN of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of PKIN. Such compounds may include agonists, antagonists, or partial or
- 15 inverse agonists. In one embodiment, an assay is performed under conditions permissive for PKIN activity, wherein PKIN is combined with at least one test compound, and the activity of PKIN in the presence of a test compound is compared with the activity of PKIN in the absence of the test compound. A change in the activity of PKIN in the presence of the test compound is indicative of a compound that modulates the activity of PKIN. Alternatively, a test compound is combined with an
- 20 in vitro or cell-free system comprising PKIN under conditions suitable for PKIN activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of PKIN may do so indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

- In another embodiment, polynucleotides encoding PKIN or their mammalian homologs may
- 25 be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the
- 30 gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic

Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential
5 therapeutic or toxic agents.

Polynucleotides encoding PKIN may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al.
10 (1998) Science 282:1145-1147).

Polynucleotides encoding PKIN can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a polynucleotide encoding PKIN is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the
15 blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress PKIN, e.g., by secreting PKIN in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

20 Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of PKIN and human kinases. In addition, the expression of PKIN is closely associated with cancer, diseased, proliferative, cardiac, tumorous, and digestive tissues, degenerative diseases of the brain, suggesting that PKIN plays a role in necrotic disorders affecting the central nervous system, and neuronal tissues (e.g. brain and spinal cord, see Table 6). Therefore, PKIN
25 appears to play a role in maintenance and potentially the neoplastic transformation of cells of the central nervous system, and in cancer, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders. In the treatment of disorders associated with increased PKIN expression or activity, it is desirable to decrease the expression or activity of PKIN. In the treatment of disorders associated with decreased PKIN expression or activity, it is
30 desirable to increase the expression or activity of PKIN.

Therefore, in one embodiment, PKIN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN. Examples of such disorders include, but are not limited to, a cancer, such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in

- particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, leukemias such as multiple myeloma and lymphomas such as Hodgkin's disease; an immune disorder, such as acquired
- 5 immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins,
- 10 erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus,
- 15 systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria,
- 20 polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, renal tubular acidosis, anemia,
- 25 Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea
- 30 and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure,
- 35 ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease,

degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a lipid disorder such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such as Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatosis, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipoid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity.

In another embodiment, a vector capable of expressing PKIN or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified PKIN in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of PKIN may be

administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PKIN including, but not limited to, those listed above.

In a further embodiment, an antagonist of PKIN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PKIN. Examples of such disorders include, but are not limited to, those cancers, immune disorders, disorders affecting growth and development, cardiovascular diseases, and lipid disorders described above. In one aspect, an antibody which specifically binds PKIN may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express PKIN.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding PKIN may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PKIN including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of PKIN may be produced using methods which are generally known in the art. In particular, purified PKIN may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind PKIN. Antibodies to PKIN may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with PKIN or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to PKIN have an amino acid sequence consisting of at least about 5 amino acids, and generally will

consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of PKIN amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

- 5 Monoclonal antibodies to PKIN may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) *Nature* 256:495-497; Kozbor, D. et al. (1985) *J. Immunol. Methods* 81:31-42; Cote, R.J. et al. (1983) *Proc. Natl. Acad. Sci. USA* 80:2026-2030; and
10 Cole, S.P. et al. (1984) *Mol. Cell Biol.* 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) *Proc. Natl. Acad. Sci. USA* 81:6851-6855; Neuberger, M.S. et al. (1984) *Nature* 312:604-608; and Takeda,
15 S. et al. (1985) *Nature* 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce PKIN-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) *Proc. Natl. Acad. Sci. USA* 88:10134-10137.)

- 20 Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:3833-3837; Winter, G. et al. (1991) *Nature* 349:293-299.)

Antibody fragments which contain specific binding sites for PKIN may also be generated.
25 For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) *Science* 246:1275-1281.)

- 30 Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between PKIN and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies
35 reactive to two non-interfering PKIN epitopes is generally used, but a competitive binding assay may

also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for PKIN. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of PKIN-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple PKIN epitopes, represents the average affinity, or avidity, of the antibodies for PKIN. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular PKIN epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the PKIN-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of PKIN, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of PKIN-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding PKIN, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding PKIN. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding PKIN. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995)

9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, *supra*; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding PKIN may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) *Science* 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) *Science* 270:475-480; Bordignon, C. et al. (1995) *Science* 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) *Cell* 75:207-216; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:643-666; Crystal, R.G. et al. (1995) *Hum. Gene Therapy* 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) *Science* 270:404-410; Verma, I.M. and N. Somia (1997) *Nature* 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) *Nature* 335:395-396; Poeschla, E. et al. (1996) *Proc. Natl. Acad. Sci. USA.* 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in PKIN expression or regulation causes disease, the expression of PKIN from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in PKIN are treated by constructing mammalian expression vectors encoding PKIN and introducing these vectors by mechanical means into PKIN-deficient cells. Mechanical transfer technologies for use with cells *in vivo* or *ex vitro* include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) *Annu. Rev. Biochem.* 62:191-217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J-L. and H. Récipon (1998) *Curr. Opin. Biotechnol.* 9:445-450).

Expression vectors that may be effective for the expression of PKIN include, but are not

limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). PKIN may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Gossen, M. et al. (1995) *Science* 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the ec dysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding PKIN from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to PKIN expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding PKIN under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-

cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et al. (1997) *Blood* 89:2259-2267; Bonyhadi, M.L. (1997) *J. Virol.* 71:4707-4716; Ranga, U. et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:1201-1206; Su, L. (1997) *Blood* 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding PKIN to cells which have one or more genetic abnormalities with respect to the expression of PKIN. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) *Transplantation* 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) *Annu. Rev. Nutr.* 19:511-544 and Verma, I.M. and N. Somia (1997) *Nature* 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding PKIN to target cells which have one or more genetic abnormalities with respect to the expression of PKIN. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing PKIN to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) *Exp. Eye Res.* 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) *J. Virol.* 73:519-532 and Xu, H. et al. (1994) *Dev. Biol.* 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to

deliver polynucleotides encoding PKIN to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and K.-J. Li (1998) *Curr. Opin. Biotechnol.* 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for PKIN into the alphavirus genome in place of the capsid-coding region results in the production of a large number of PKIN-coding RNAs and the synthesis of high levels of PKIN in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) *Virology* 228:74-83). The wide host range of alphaviruses will allow the introduction of PKIN into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding PKIN.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides,

corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

5 Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding PKIN. Such DNA sequences may be incorporated into a wide variety of vectors
10 with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3'
15 ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous
20 endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding PKIN. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides,
25 transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased PKIN expression or activity, a compound which specifically inhibits expression of the polynucleotide
30 encoding PKIN may be therapeutically useful, and in the treatment of disorders associated with decreased PKIN expression or activity, a compound which specifically promotes expression of the polynucleotide encoding PKIN may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method
35 commonly known in the art, including chemical modification of a compound known to be effective in

altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding PKIN is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding PKIN are assayed by any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding PKIN. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun. 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruice, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruice, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient. Excipients may include, for example, sugars, starches, celluloses, gums, and proteins.

Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of PKIN, antibodies to PKIN, and mimetics, agonists, antagonists, or inhibitors of PKIN.

The compositions utilized in this invention may be administered by any number of routes
5 including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the
10 case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration
15 without needle injection, and obviates the need for potentially toxic penetration enhancers.

Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

Specialized forms of compositions may be prepared for direct intracellular delivery of
20 macromolecules comprising PKIN or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, PKIN or a fragment thereof may be joined to a short cationic N-terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et
25 al. (1999) Science 285:1569-1572).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and
30 routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example PKIN or fragments thereof, antibodies of PKIN, and agonists, antagonists or inhibitors of PKIN, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by
35 calculating the ED₅₀ (the dose therapeutically effective in 50% of the population) or LD₅₀ (the dose

lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind PKIN may be used for the diagnosis of disorders characterized by expression of PKIN, or in assays to monitor patients being treated with PKIN or agonists, antagonists, or inhibitors of PKIN. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for PKIN include methods which utilize the antibody and a label to detect PKIN in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring PKIN, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of PKIN expression. Normal or standard values for PKIN expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to PKIN under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of PKIN expressed in subject,

control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding PKIN may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of PKIN may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of PKIN, and to monitor regulation of PKIN levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding PKIN or closely related molecules may be used to identify nucleic acid sequences which encode PKIN. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding PKIN, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the PKIN encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:19-36 or from genomic sequences including promoters, enhancers, and introns of the PKIN gene.

Means for producing specific hybridization probes for DNAs encoding PKIN include the cloning of polynucleotide sequences encoding PKIN or PKIN derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding PKIN may be used for the diagnosis of disorders associated with expression of PKIN. Examples of such disorders include, but are not limited to, a cancer, such as adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, leukemias such as multiple myeloma and lymphomas such as Hodgkin's disease; an immune disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis,

- autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis,
- 5 glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner
- 10 syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a growth and developmental disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma,
- 15 leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus, renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy,
- 20 gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and
- 25 sensorineural hearing loss; a cardiovascular disease, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease,
- 30 degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation, congenital lung
- 35 anomalies, atelectasis, pulmonary congestion and edema, pulmonary embolism, pulmonary

hemorrhage, pulmonary infarction, pulmonary hypertension, vascular sclerosis, obstructive pulmonary disease, restrictive pulmonary disease, chronic obstructive pulmonary disease, emphysema, chronic bronchitis, bronchial asthma, bronchiectasis, bacterial pneumonia, viral and mycoplasmal pneumonia, lung abscess, pulmonary tuberculosis, diffuse interstitial diseases, pneumoconioses, sarcoidosis, idiopathic pulmonary fibrosis, desquamative interstitial pneumonitis, hypersensitivity pneumonitis, pulmonary eosinophilia bronchiolitis obliterans-organizing pneumonia, diffuse pulmonary hemorrhage syndromes, Goodpasture's syndromes, idiopathic pulmonary hemosiderosis, pulmonary involvement in collagen-vascular disorders, pulmonary alveolar proteinosis, lung tumors, inflammatory and noninflammatory pleural effusions, pneumothorax, pleural tumors, drug-induced lung disease, radiation-induced lung disease, and complications of lung transplantation; and a lipid disorder such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such as Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM₂ gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatosis, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipoid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia, Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity. The polynucleotide sequences encoding PKIN may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered PKIN expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding PKIN may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding PKIN may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding PKIN in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of PKIN, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding PKIN, under conditions suitable for hybridization or amplification.

5 Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

10 Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

15 With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development
20 or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding PKIN may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding PKIN, or a fragment of a polynucleotide complementary to the polynucleotide encoding
25 PKIN, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding PKIN may be used to detect single nucleotide polymorphisms (SNPs). SNPs are
30 substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding PKIN are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example,
35 from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause

differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

Methods which may also be used to quantify the expression of PKIN include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C. et al. (1993) *Anal. Biochem.* 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, PKIN, fragments of PKIN, or antibodies specific for PKIN may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by

quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of
5 transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines,
10 biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental
15 compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share
20 those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for
25 comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at
30 <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of
35 the present invention, so that transcript levels corresponding to the polynucleotides of the present

invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, supra). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for PKIN to quantify the levels of PKIN expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) Anal. Biochem. 270:103-111; Mendoz, L.G. et al. (1999) Biotechniques 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson,

N.L. and J. Seilhamer (1997) Electrophoresis 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding PKIN may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1

constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355; Price, C.M. (1993) *Blood Rev.* 7:127-134; and Trask, B.J. (1991) *Trends Genet.* 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, for example, Lander, E.S. and D. Botstein (1986) *Proc. Natl. Acad. Sci. USA* 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding PKIN on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) *Nature* 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, PKIN, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between PKIN and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with PKIN, or fragments thereof, and washed. Bound PKIN is then detected by methods well known in the art. Purified PKIN can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PKIN specifically compete with a test compound for binding PKIN. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PKIN.

5 In additional embodiments, the nucleotide sequences which encode PKIN may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding
10 description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific
15 embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/199,021, U.S. Ser. No. 60/200,226, U.S. Ser. No. 60/202,339, U.S. Ser. No. 60/203,505, U.S. Ser. No. 60/205,654, U.S. Ser. No. 60/207,739, and U.S. Ser. No. 60/208,795,
20 are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database
25 (Incyte Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium
30 acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was
35 isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA

purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the
5 recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-
1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column
10 chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUEScript plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto CA), or derivatives thereof. Recombinant plasmids were transformed into competent E. coli cells
15 including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectromAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by in vivo excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using
20 at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

25 Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence
30 scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal
35 cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the

MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) Curr. Opin. Struct. Biol. 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate
5 references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

The programs described above for the assembly and analysis of full length polynucleotide
10 and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:19-36. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 4.

IV. Identification and Editing of Coding Sequences from Genomic DNA

Putative human kinases were initially identified by running the Genscan gene identification
15 program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) *J. Mol. Biol.* 268:78-94, and Burge, C. and S. Karlin (1998) *Curr. Opin. Struct. Biol.* 8:346-354). The program concatenates predicted exons to form an assembled cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a
20 FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode human kinases, the encoded polypeptides were analyzed by querying against PFAM models for kinases. Potential human kinases were also identified by homology to Incyte cDNA sequences that had been annotated as kinases. These selected Genscan-predicted sequences
25 were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing evidence for transcription. When Incyte cDNA coverage was available,
30 this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding sequences.

35 V. Assembly of Genomic Sequence Data with cDNA Sequence Data

"Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence. Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants. Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbprl public databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

"Stretched" Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore "stretched" or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to determine whether it contained a complete gene.

VI. Chromosomal Mapping of PKIN Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:19-36 were compared with

sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched SEQ ID NO:19-36 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Génethon were used to determine if any of the clustered sequences had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Génethon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

In this manner, SEQ ID NO:24 was mapped to chromosome 2 within the interval from 92.30 to 103.1 centiMorgans, SEQ ID NO:25 was mapped to chromosome 11 within the interval from 104.8 to 117.9 centiMorgans, SEQ ID NO:33 was mapped to chromosome 8 within the interval from 25.8 to 40.3 centiMorgans, SEQ ID NO:23 was mapped to chromosome 9 within the interval from 101.20 to 104.90 centiMorgans, to chromosome 10 within the interval from 145.20 to 156.60 centiMorgans, and to chromosome 19 within the interval from 69.90 to 81.20 centiMorgans. More than one map location is reported for SEQ ID NO:23, indicating that sequences having different map locations were assembled into a single cluster. This situation occurs when sequences having strong similarity, but not complete identity, are assembled into a single cluster.

VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel (1995) supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is

much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum \{length(Seq. 1), length(Seq. 2)\}}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding PKIN are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding PKIN. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of PKIN Encoding Polynucleotides

Full length polynucleotide sequences were also produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was
5 synthesized to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

10 Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$,
15 and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2:
20 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar,
25 Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

30 The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones
35 were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham

Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

- 5 The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA
- 10 recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

- In like manner, full length polynucleotide sequences are verified using the above procedure or
- 15 are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling and Use of Individual Hybridization Probes

- Hybridization probes derived from SEQ ID NO:19-36 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base
- 20 pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 µCi of [γ -³²P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a
- 25 SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

- The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon
- 30 membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and compared.

- 35 **X. Microarrays**

The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned technologies should be uniform and solid with a non-porous surface (Skena (1999), 5 supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may contain any appropriate number of elements. (See, e.g., 10 Skena, M. et al. (1995) *Science* 270:467-470; Shalon, D. et al. (1996) *Genome Res.* 6:639-645; Marshall, A. and J. Hodgson (1998) *Nat. Biotechnol.* 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The 15 array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of 20 complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and 25 poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/μl oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/μl RNase inhibitor, 500 μM dATP, 500 μM dGTP, 500 μM dTTP, 40 μM dCTP, 40 μM dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with 30 GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85°C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc.

(CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14 μ l 5X SSC/0.2% SDS.

5 Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5
10 μ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR
15 Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 μ l of the array element DNA, at an average
20 concentration of 100 ng/ μ l, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate
25 buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 μ l of sample mixture consisting of 0.2 μ g each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample
30 mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 μ l of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash

buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an
5 Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines
at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is
focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide
containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-
scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a
10 resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially.
Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477,
Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate
filters positioned between the array and the photomultiplier tubes are used to filter the signals. The
15 emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is
typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source,
although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a
cDNA control species added to the sample mixture at a known concentration. A specific location on
20 the array contains a complementary DNA sequence, allowing the intensity of the signal at that
location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples
from different sources (e.g., representing test and control cells), each labeled with a different
fluorophore, are hybridized to a single array for the purpose of identifying genes that are
differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the
25 two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital
(A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC
computer. The digitized data are displayed as an image where the signal intensity is mapped using a
linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high
30 signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and
measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping
emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each
spot is centered in each element of the grid. The fluorescence signal within each element is then

integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

Sequences complementary to the PKIN-encoding sequences, or any parts thereof, are used to
5 detect, decrease, or inhibit expression of naturally occurring PKIN. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of PKIN. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent
10 promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the PKIN-encoding transcript.

XII. Expression of PKIN

Expression and purification of PKIN is achieved using bacterial or virus-based expression systems. For expression of PKIN in bacteria, cDNA is subcloned into an appropriate vector
15 containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express PKIN upon induction with isopropyl beta-D-
20 thiogalactopyranoside (IPTG). Expression of PKIN in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding PKIN by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong
25 polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

30 In most expression systems, PKIN is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham
35 Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from

PKIN at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, 5 supra, ch. 10 and 16). Purified PKIN obtained by these methods can be used directly in the assays shown in Examples XVI, XVII, and XVIII where applicable.

XIII. Functional Assays

PKIN function is assessed by expressing the sequences encoding PKIN at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression 10 vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a 15 marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate 20 the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; 25 alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of PKIN on gene expression can be assessed using highly purified populations 30 of cells transfected with sequences encoding PKIN and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. 35 Expression of mRNA encoding PKIN and other genes of interest can be analyzed by northern analysis

or microarray techniques.

XIV. Production of PKIN Specific Antibodies

PKIN substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to
5 immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the PKIN amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well
10 described in the art. (See, e.g., Ausubel, 1995, *supra*, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using Fmoc chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the
15 oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide and anti-PKIN activity by, for example, binding the peptide or PKIN to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XV. Purification of Naturally Occurring PKIN Using Specific Antibodies

20 Naturally occurring or recombinant PKIN is substantially purified by immunoaffinity chromatography using antibodies specific for PKIN. An immunoaffinity column is constructed by covalently coupling anti-PKIN antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

25 Media containing PKIN are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PKIN (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/PKIN binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and PKIN is collected.

30 XVI. Identification of Molecules Which Interact with PKIN

PKIN, or biologically active fragments thereof, are labeled with ^{125}I Bolton-Hunter reagent. (See, e.g., Bolton A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled PKIN, washed, and any wells with labeled PKIN complex are assayed. Data obtained using different concentrations
35 of PKIN are used to calculate values for the number, affinity, and association of PKIN with the

candidate molecules.

Alternatively, molecules interacting with PKIN are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) *Nature* 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

- 5 PKIN may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT) which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XVII. Demonstration of PKIN Activity

- 10 Generally, protein kinase activity is measured by quantifying the phosphorylation of a protein substrate by PKIN in the presence of gamma-labeled ^{32}P -ATP. PKIN is incubated with the protein substrate, ^{32}P -ATP, and an appropriate kinase buffer. The ^{32}P incorporated into the substrate is separated from free ^{32}P -ATP by electrophoresis and the incorporated ^{32}P is counted using a radioisotope counter. The amount of incorporated ^{32}P is proportional to the activity of PKIN. A
15 determination of the specific amino acid residue phosphorylated is made by phosphoamino acid analysis of the hydrolyzed protein.

- In one alternative, protein kinase activity is measured by quantifying the transfer of gamma phosphate from adenosine triphosphate (ATP) to a serine, threonine or tyrosine residue in a protein substrate. The reaction occurs between a protein kinase sample with a biotinylated peptide substrate
20 and gamma ^{32}P -ATP. Following the reaction, free avidin in solution is added for binding to the biotinylated ^{32}P -peptide product. The binding sample then undergoes a centrifugal ultrafiltration process with a membrane which will retain the product-avidin complex and allow passage of free gamma ^{32}P -ATP. The reservoir of the centrifuged unit containing the ^{32}P -peptide product as retentate is then counted in a scintillation counter. This procedure allows assay of any type of protein kinase
25 sample, depending on the peptide substrate and kinase reaction buffer selected. This assay is provided in kit form (ASUA, Affinity Ultrafiltration Separation Assay, Transbio Corporation, Baltimore MD, U.S. Patent No. 5,869,275). Suggested substrates and their respective enzymes are as follows: Histone H1 (Sigma) and p34^{cdc2}kinase, Annexin I, Angiotensin (Sigma) and EGF receptor kinase, Annexin II and *src* kinase, ERK1 & ERK2 substrates and MEK, and myelin basic protein and
30 ERK (Pearson, J.D. et al. (1991) *Methods Enzymol.* 200:62-81).

In another alternative, protein kinase activity of PKIN is demonstrated *in vitro* in an assay containing PKIN, 50 μl of kinase buffer, 1 μg substrate, such as myelin basic protein (MBP) or synthetic peptide substrates, 1 mM DTT, 10 μg ATP, and 0.5 μCi [γ - ^{32}P]ATP. The reaction is incubated at 30°C for 30 minutes and stopped by pipetting onto P81 paper. The unincorporated [γ -

³²P]ATP is removed by washing and the incorporated radioactivity is measured using a radioactivity scintillation counter. Alternatively, the reaction is stopped by heating to 100°C in the presence of SDS loading buffer and visualized on a 12% SDS polyacrylamide gel by autoradiography. Incorporated radioactivity is corrected for reactions carried out in the absence of PKIN or in the presence of the inactive kinase, K38A.

In yet another alternative, adenylate kinase or guanylate kinase activity may be measured by the incorporation of ³²P from gamma-labeled ³²P-ATP into ADP or GDP using a gamma radioisotope counter. The enzyme, in a kinase buffer, is incubated together with the appropriate nucleotide mono-phosphate substrate (AMP or GMP) and ³²P-labeled ATP as the phosphate donor. The reaction is incubated at 37°C and terminated by addition of trichloroacetic acid. The acid extract is neutralized and subjected to gel electrophoresis to separate the mono-, di-, and triphosphonucleotide fractions. The diphosphonucleotide fraction is cut out and counted. The radioactivity recovered is proportional to the enzyme activity.

In yet another alternative, other assays for PKIN include scintillation proximity assays (SPA), scintillation plate technology and filter binding assays. Useful substrates include recombinant proteins tagged with glutathione transferase, or synthetic peptide substrates tagged with biotin. Inhibitors of PKIN activity, such as small organic molecules, proteins or peptides, may be identified by such assays.

XVIII. Enhancement/Inhibition of Protein Kinase Activity

Agonists or antagonists of PKIN activation or inhibition may be tested using assays described in section XVII. Agonists cause an increase in PKIN activity and antagonists cause a decrease in PKIN activity.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
2890544	1	2890544CD1	19	2890544CB1
7472693	2	7472693CD1	20	7472693CB1
3107952	3	3107952CD1	21	3107952CB1
5544420	4	5544420CD1	22	5544420CB1
7472832	5	7472832CD1	23	7472832CB1
1551456	6	1551456CD1	24	1551456CB1
2589355	7	2589355CD1	25	2589355CB1
4357117	8	4357117CD1	26	4357117CB1
5511992	9	5511992CD1	27	5511992CB1
7474560	10	7474560CD1	28	7474560CB1
7474602	11	7474602CD1	29	7474602CB1
7475509	12	7475509CD1	30	7475509CB1
7475491	13	7475491CD1	31	7475491CB1
2192119	14	2192119CD1	32	2192119CB1
7474496	15	7474496CD1	33	7474496CB1
1834248	16	1834248CD1	34	1834248CB1
71584520	17	71584520CD1	35	71584520CB1
7475538	18	7475538CD1	36	7475538CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
1	2890544CD1	g5305331	0	protein kinase Myak-L [Mus musculus]
2	7472693CD1	g790790	2.4e-144	cam kinase I [Homo sapiens]
3	3107952CD1	g1403532	2.3e-226	KIS protein kinase [Rattus norvegicus] (Maucuer, A. et al. (1997))
4	55444420CD1	g205278	6.4e-293	J. Biol. Chem. 272: 23151-23156) male germ cell-associated kinase (mak) [Rattus norvegicus] (Matsushime, H. et al. (1990)) Mol. Cell. Biol. 10: 2261-2268)
5	7472832CD1	g438373	0.0	protein kinase C mu [Homo sapiens] (Johannes, F.J. et al. (1994)) J. Biol. Chem. 269: 6140-6148)
6	1551456CD1	g4099088	3.8e-26	[Arabidopsis thaliana] SNF1 family protein kinase
7	2589355CD1	g6760436	1.2e-144	[Gallus gallus] gin-induced kinase
8	4357117CD1	g6552404	2.4e-199	[Rattus norvegicus] DLG6 alpha
9	5511992CD1	g971420	3.9e-231	mixed lineage kinase 2 [Homo sapiens]
9	5511992CD1	g12005724	0	Dorow, D.S. et al., (1995) Eur. J. Biochem. 234:492-500 [5' incm] [Homo sapiens] mixed lineage kinase MLX1
10	7474560CD1	g4691541	7.3e-102	Adenylate kinase 5 [Homo sapiens]. Van Rompay, A.R. et al. (1999) Identification of a novel human adenylate kinase cDNA cloning, expression analysis, chromosome localization and characterization of the recombinant protein, Eur. J. Biochem. 261:509-516.
11	7474602CD1	g439614	8.9e-145	Cam-like protein kinase [Rattus norvegicus]. Cho, F.S. et al. (1994) Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase I, Biochim. Biophys. Acta 1224:156-160.

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
12	7475509CD1	g28577	2.4e-112	Nucleoside-triphosphate--adenylate kinase [Homo sapiens]. Xu, G. et al. (1992) Characterization of human adenylate kinase 3 (AK3) cDNA and mapping of the AK3 pseudogene to an intron of the NF1 gene, Genomics 13:537-542.
13	7475491CD1	g2257588	1.4e-210	PCTAIRE3 [Rattus rattus]. Hirose, T. et al. (1997) PCTAIRE 2, a Cdc2-related serine/threonine kinase, is predominantly expressed in terminally differentiated neurons, Eur. J. Biochem. 249:481-488.
14	2192119CD1	g3880563	2.0e-121	Predicted using Genefinder; similar to serine/threonine kinase; cDNA [Caenorhabditis elegans]. The C.elegans Sequencing Consortium (1998) Science 282:2012-2018.
14	2192119CD1	g10442581	0	105-kDa kinase-like protein [Mus musculus] Liu, S.C.H., et al., (2000) Biochim. Biophys. Acta 1517:148-152
15	7474496CD1	g6066585	0.0	GCN2 eIF2alpha kinase [Mus musculus].
16	1834248CD1	g7595802	1.40E-252	ELKL motif kinase 2 short form [Mus musculus]
17	71584520CD1	g3927912	3.9e-157	calmodulin binding protein kinase [Fugu rubripes] Cottage, A. et al. (1999) FEBS Lett. 443: 370-374
18	7475538CD1	g4090958	9.2e-85	cell cycle related kinase [Homo sapiens]
18	7475538CD1	g9664926	0	CDK-related protein kinase PNQLARE [Mus musculus]

Table 3

SEQ ID NO.	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	2890544CD1	1210	S20 T107 T163 S211 T422 T666 S843 S853 T907 S127 T212 T508 S29 S37 T87 S113 S169 S211 S396 T441 T474 T643 S856 S910 T912 T938 S967 Y459 T1057 S1008 S1138 S1187	N57 N111 N133 N149 N262 N471 N566 N570 N1009 N1045	Protein_Kinase_Atp: L196-K219 Protein_Kinase_St: L311-L323 Eukaryotic protein kinase domain: Y190-P411 I492-V518 Tyrosine kinase catalytic domain signature PD00109B: K305-L323 PROTEIN KINASE NUCLEAR HOMEODOMAIN INTERACTING HOMEBOX DNABINDING SERINE/THREONINE SERINE/THREONINEPROTEIN: PD150874: G1030-L1210 PROTEIN KINASE DOMAIN: DM00004 P14680 371-694: V192-P509 PROTEIN KINASE DOMAIN DM00004 S57347 21-266: E24-C270 Protein_Kinase_Atp: L29-K52 Protein_Kinase_St: I140-Y152 signal_cleavage: M1-A40 Eukaryotic protein kinase domain pkinase: F23-I279 Protein kinases signatures and profile: D120-D176 Tyrosine kinase catalytic domain signature PR00109A:M98-V111 PR00109B:Y134-Y152 PR00109D: V202-E224 PROTEIN KINASE CALMODULINBINDING I CALCIUM/ CALMODULIN DEPENDENT TYPE CAM TRANSFERASE SERINE/THREONINE PROTEIN PHOSPHORYLATION PD012137: W278-L322	MOTIFS MOTIFS HMMER_PFAM BLIMPS_PRINTS BLAST_PRODROM BLAST_PRODROM BLAST_DOMO BLAST_DOMO MOTIFS MOTIFS SPSCAN HMMER_PFAM PROFILESSCAN BLIMPS_PRINTS BLAST_PRODROM
2	7472693CD1	357	S64 S102 T117 S154 S169 S251 S326 S343 Y116 Y133 S11 T45 T269	N225 N311 N332		

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
3	3107952CD1	419	S67 S117 S181 S215 S221 T244 S290 T390	N253	transmembrane domain: V223-L241 Eukaryotic protein kinase domain: W23-F304 Tyrosine kinase catalytic domain PR00109B:F148-W166 PR00109D:V223-V245 PR00109E:P273-A295 SERINE/THREONINE PROTEIN KINASE PD153748:S305-V344 SPLICING FACTOR LIKE PROTEIN PD072361:T320-G412 RIBONUCLEOPROTEIN REPEAT DM00012 A48249 299-407:P319-Y404 PROTEIN KINASE DOMAIN DM00004 P08414 44-285:R74-I293 DM00004 P32485 24-292:S48-P289 DM00004 P49657 101-409:C108-L241	HMMER HMMER_PFAM BLIMPS_PRINTS BLAST_PRODOR BLAST_PRODOR BLAST_DOMO BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
4	5544420CD1	624	T274 S424 S436 S496 S41 S179 S204 S315 S406 S451 S466 S500 S530 T6 S53 S161 T218 S388 S391 S420 S463 T475 T581 S587 T594 Y15 Y76 T571	N24 N252 N352 N384 N449 N455 N543 N569	Eukaryotic protein kinase domain Y4-F284 Tyrosine kinase catalytic domain PR00109B:F115-C133 PR00109D:I181-T203 PR00109E:A253-A275 Protein kinases signatures & profile: V101-Q153 Protein kinases ATP-binding region: L10-K33 Serine/Threonine protein kinases: F121-C133 ATP/GTP-binding site motif A (P-loop): G16-S23 KINASE SERINE/THREONINE MALE GERM CELL TRANSFERASE ATP BINDING PD024663:Q285-R624 KINASE SERINE/THREONINE ATPBINDING II PHOSPHORYLATION CASEIN ALPHA CHAIN PD002608:V160-F284 KINASE TRANSFERASE ATP BINDING SERINE/THREONINE PHOSPHORYLATION RECEPTOR TYROSINE PROTEIN PD000001:P155-F284 PROTEIN KINASE DOMAIN DM000004:Q04859 6-274:T6-A275 DM000004:I48733 6-274:T6-A275 DM000004:P43294 14-281:M7-A275 DM000004:Q00526 6-286:M7-F284	HMMER_PFBM BLIMPS_PRINTS PROFILESSCAN MOTIFS MOTIFS MOTIFS BLAST_PRODUM BLAST_PRODUM BLAST_PRODUM BLAST_PRODUM BLAST_PRODUM
5	7472832CD1	878	S197 S396 S797 S75 S111 T130 T218 S225 S333 S353 S362 T398 S408 T573 T589 T812 T853 S145 S206 T247 S387 T391 T392 T412 T434 S604 S641 S706 Y87	N187 N431 N432 N454 N473 N729	Eukaryotic protein kinase domain: I551-L807 Phorbol esters/diacylglycerol binding H139-C188 H265-C314 PH domain: T398-V478 Protein kinases signatures & profile: L650-S706	HMMER_PFBM HMMER_PFBM HMMER_PFBM PROFILESSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5					Phorbol esters/diacylglycerol binding F151-S214 C278-A339	PROFILES CAN
					Tyrosine kinase catalytic domain: PR00109B:H664-L682 PR00109D:L732-D754	BLIMPS_PRINTS
					Diacylglycerol/phorbol-esterase PR00008B:C152-G161 PR00008C:Q291-C302 PR00008D:H303-L315	BLIMPS_PRINTS
					KINASE PHORBOLESTER C MU SERINE/THREONINE NPKCMU ATP BINDING PD039353:D323-V478 PD031784:V45-P138 PD027900:L807-L878	BLAST_PROD OM
					KINASE PHORBOLESTER BINDING TRANSFERASE SERINE/THREONINE ZINC ATPBINDING C DUPLICATION PD000215:H265-C314	BLAST_PROD OM
					Protein kinases signatures and profile (protein_kinase_tyr.prf): R826-A877	BLAST_PROD OM
					PROTEIN KINASE DOMAIN DM00004 A53215 585-829:P553-V798 DM00004 I48719 591-835:P553-V798 DM04692 A37237 1-676:V556-S771 M04692 P05773 1-672:V556-P845	BLAST_DOMO
					Phorbol esters / diacylglycerol binding domain: H139-C188 H265-C314	MOTIFS
					Protein kinases ATP-binding region signature: L557-K580	MOTIFS
					Serine/threonine protein kinases active-site signature: I670-L682	MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
6	1551456CD1	440	S11 S175 T74 S85 S230 T297 S361 S365 S376 S396 T426 S11 S19 S131 S155 T214 S251 Y68 Y378		Eukaryotic protein kinase domain: L164-E331 Tyrosine kinase signature: A192-L210, S260-S282 PROTEIN KINASE DOMAIN DM00004 P34244 82-359: Y167-L324 Protein kinase motif: I198-L210 PROTEIN KINASE DOMAIN DM00004 P27448 58-297: G25-I259 Serine/Threonine protein kinases active-site signature Protein_Kinase_St: I135-L147 Eukaryotic protein kinase domain pkinase: S24-M268 Protein kinases signatures and profile protein_kinase_tyr.prf: Y90-G167 Tyrosine kinase catalytic site PR00109: T93-A106, Y129-L147, L195-P217 SH3 domain signature PR00452: C147-RJ59, A115-Q130, D132-I141 PROTEIN DOMAIN SH3 KINASE GUANYLATE TRANSFERASE ATPBINDING REPEAT GMP MEMBRANE PD001338: T267-Q360 GUANYLATE KINASE DM00755 A57653 370- 570: P228-P431 PDZ signaling molecule domain PDZ: I3-V83 Guanylate kinase Guanylate_kin: T268-Y372 Guanylate kinase protein BL00856: V264-V284, L292-R339	HMMER-PFAM BLIMPS-PRINTS BLAST-DOMO MOTIFS HMMER-PFAM PROFILES SCAN BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO HMMER-PFAM HMMER-PFAM BLIMPS-BLOCKS
7	2589355CD1	923	Y104 Y676 T258 S355 T481 S584 T38 S125 S289 T356 S391 T447 S448 T455 T481 S500 S512 T875 S890 T17 S254 S336 T417 S472 S531 S542 S551 S564 S576 S667	N112 N317		MOTIFS BLAST-DOMO MOTIFS HMMER-PFAM
8	4357117CD1	442	T16 T267 T270 S295 S361 S142 S229 S178 S180 T311 S408 S437 Y294 Y304 Y346	N406		BLIMPS-PRINTS BLAST-PRODOM BLAST-DOMO HMMER-PFAM HMMER-PFAM BLIMPS-BLOCKS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
9	5511992CD1	1046	T72 T112 S118 S223 S276 T294 S603 S707 S770 S781 S814 S880 T913 S531 T777 S89 T135 T363 T394 T395 T436 S599 S606 S636 T644 S808 S821 S834 T884 T919 S923 S966 S972 S983 T984 Y325	N813 N862 N964	Receptor tyrosine kinase BL00240: E290-V337, V337-I389 Receptor tyrosine kinase BL00239: E181-P228, L232-I254, W291-R340, L345-I389 Receptor tyrosine kinase BL00790: I154-C207, S298-W330, L356-M404 Protein kinase signature and profile protein_kinase_tyr.prf: L232-T294 Tyrosine kinase catalytic site PR00109: M210-S223, D248-I266, G301-I311, S320-I342, C364-F386 SH3 domain signature PR00452: P55-A65, D69-K84, D91-N100, R102-R114 SH3 domain: P55-R114 Eukaryotic protein kinase domain pkinase: L134-L393 KINASE DOMAIN SH3 MIXED LINEAGE SERINE/THREONINE WITH LEUCINE ZIPPER PROLINE PD024997: I396-A741 PROTEIN KINASE DOMAIN DM00004 A53800 119-368: I136-F386 Protein kinases ATP-binding region signature Protein_Kinase_Atp: I140-K161 Serine/Threonine protein kinases active-site signature Protein_Kinase_St: I254-I266	BLIMPS-BLOCKS BLIMPS-BLOCKS BLIMPS-BLOCKS PROFILES-SCAN BLIMPS-PRINTS BLIMPS-PRINTS HMMER-PFAM HMMER-PFAM BLAST-PRODOM BLAST-DOMO MOTIFS MOTIFS

Table 3 (cont.)

[illegible]

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
12	7475509CD1	224	S16, S75, T118, S124, S132, T201,		ADENYLATE KINASE: DM00290 P27144 1-125: M1-R126. Adenylate kinase signature: PR00094A: V9-C22; PR00094B: G37-G51; PR00094C: W85-D101; PR00094D: Q159-Y174; PR00094E: D176-V190. Shikimate kinase family: PR01100A: A8-Q23; PR01100E: D107-S124 (p<0.0028). Adenylate Kinase Motif: W85-Q96. KINASE ADENYLATE TRANSFERASE, ATP-BINDING ATP/AMP TRANSPHOSPHORYLASE ISOENZYME, PROTEIN 3D-STRUCTURE MITOCHONDRION: PD000657: I10-V190. Adenylate kinase: I10-V190 Adenylate kinase protein: BL00113A: V9-I25; BL00113B: H33-E76; BL00113C: R80-L94; BL00113D: S132-D162. Adenylate kinase signature (adenylate_kinase.prf): V64-F116. PROTEIN KINASE DOMAIN: DM00004 Q04899 122-392: V173-A444, KINASE SERINE/THREONINE PROTEIN TRANSFERASE ATP-BINDING DOMAIN - PCTAIRE1, PCTAIRE2, PCTAIRE3, CRK5 ALTERNATIVE PD007333: D120-T171 Tyrosine kinase catalytic domain: PR00109B: Y283-I301 Protein kinases signatures and profile (protein_kinase_tyr.prf): D235-A317 Eukaryotic protein kinase domain (pkinae): Y172-F453, Protein kinases ATP-binding region signature: L178-K201 Serine/Threonine protein kinases active-site signature: I289-I301	BLAST-DOMO BLIMPS-PRINTS BLIMPS-PRINTS MOTIFS BLAST-PRODOM HMMER-PFAM BLIMPS-BLOCKS PROFILES-SCAN BLAST-DOMO BLAST-PRODOM BLIMPS-PRINTS PROFILES-SCAN HMMER-PFAM MOTIFS MOTIFS
13	7475491CD1	502	S12, T20, S24, S60, S64, S87, T104, S122, S126, S156, S160, Y183, T232, T239, T348, T364, T373, T387, S455, S471, S500,			

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
14	2192119CD1	791	T39, T70, T85, S193, S269, T319, S342, S359, T361, T408, S462, S499, S521, S535, S539, T545, T581, T610, T617, S622, S662, S668, S677, S693, S716, S726, S737, Y184	N447	PROTEIN KINASE DOMAIN DM00004 P52304 27-267: K69-P254 (p > 1.3e-06)	BLAST-DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
15	7474496CD1	1651	T65, T82, S108, S144, S210, T215, S216, S247, S250, T329, T346, T409, S414, T441, S450, T478, S553, S569, T581, S690, S709, T715, S722, S732, S733, S755, S757, T811, T824, S882, S917, T945, S947, S961, T993, T1022, S1038, S1059, T1062, T1182, T1234, T1238, S1397, T1418, S1437, S1457, S1572, T1475, S1547, T1548, T1604, S1641, Y256, Y821, Y840, Y1626	N100, N245, 1057, 1197, 1203, 1248, 1416, 1520, 1602	PROTEIN KINASE DOMAIN: DM00004 P15442 645-902: S732-A994, EUKARYOTIC INITIATION FACTOR KINASE (EIF2 ALPHA): P0156018: D13-D219 Tyrosine kinase catalytic domain: PR00109B: Y840-L858 Protein kinases signatures and profile (protein_kinase_tyr.prf): R826-A877 Eukaryotic protein kinase domain (pkinese): K335-D446; F592-P664; Y799-L1003 Protein kinases ATP-binding region signature: L598-K621 Serine/Threonine protein kinases active-site signature: M846-L858 Eukaryotic protein kinase domain: K335-D446; P504-I541; F592-P664; Y799-L1003 Protein kinases signatures and profile (protein_kinase_tyr.prf): R826-A877 Tyrosine kinase catalytic domain: PR00109B: Y840-L858 Protein kinases ATP-binding region signature: L598-K621 Serine/Threonine protein kinases active-site signature: M846-L858	BLAST-DOMO BLAST-PRODOM BLIMPS-PRINTS PROFILES-SCAN HMMER-PFAM MOTIFS MOTIFS HMMER-PFAM PROFILE-SCAN BLIMPS-PRINTS MOTIFS MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
16	1834248CD1	752	S139 S2 S210 S23 S27 S34 S354 S399 S423 S441 S458 S48 S494 S661 S666 S710 T127 T281 T300 T323 T332 T344 T507 T511 T515 T536 T564 T620 T624 T81	N395 N532	Eukaryotic protein kinase domain: Y59-I310, Tyrosine kinase catalytic domain PR00109A: M135-V148 PR00109B: Y171-L189 PR00109D: V237-H259 Protein kinases signatures and profile protein_kinase_tyr.prf: Y132-S210 Protein kinases ATP-binding region: Protein_Kinase_Atp: I65-K88 Serine/Threonine protein kinases active-site Protein_Kinase_St: I177-L189 KINASE SERINE/THREONINE TRANSFERASE ATP BINDING PROTEIN EMK P78 CDC25C PD008571: S412-E632 KINASE SERINE/THREONINE TRANSFERASE ATP BINDING PROTEIN PAR1 KP78 EMK PD005838: I310-R410 KINASE SERINE/THREONINE TRANSFERASE ATP BINDING KINL EMK PAR1 PD004300: E650-L752 KINASE TRANSFERASE ATP BINDING SERINE/ THREONINE PHOSPHORYLATION RECEPTOR TYROSINE PD000001: Y59-Y137 PROTEIN KINASE DOMAIN DM00004 P27448 58-297:L61-L301 DM00004 I48609 55-294:L61-L301 DM00004 Q05512 55-294:L61-L301 DM00004 JC1446 20-261:R60-L301	HMMER_PFAM BLIMPS_PRINTS PROFILES SCAN MOTIFS MOTIFS BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
17	71584520CD1	501	S118 S138 S292 S341 S364 S482 S483 S495 T103 T21 T276 T422 T46 T470 T51 T7 T91 Y135 Y491		Eukaryotic protein kinase domain pkinase: E37-I286 Tyrosine kinase catalytic domain PR00109B: Y135-Y153 PR00109D: V201-E223 CALMODULIN BINDING PROTEIN PD059862: G368-V443 PROTEIN KINASE CALMODULIN BINDING I CALCIUM/CALMODULIN DEPENDENT TYPE CAM TRANSFERASE SERINE/THREONINE PROTEIN PHOSPHORYLATION PD012137: W285-A335 CALMODULIN BINDING PROTEIN PD050813: M1-E34 PROTEIN KINASE DOMAIN DM00004 S57347 21-266:D25-T276 DM00004 P08414 44-285:I38-T276 DM00004 P11798 15-261:C36-A277 DM00004 A44412 16-262:F35-A277	HMMER_Pfam BLIMPS_PRINTS BLAST_PRODOR BLAST_PRODOR BLAST_PRODOR BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
18	7475538CD1	346	S241 Y176 Y215		Eukaryotic protein kinase domain pkinase: Y4-F288, Tyrosine kinase catalytic domain PR0109B: F117-I135 Protein kinases signatures and profile protein_kinase_tyr.prf: A69-D155 Protein kinases ATP-binding region signature Protein_Kinase_Atp: I10-K33 Serine/Threonine protein kinases active-site Protein_Kinase_St: I123-I135 KINASE TRANSFERASE SERINE/THREONINE ATP BINDING II PHOSPHORYLATION CASEIN ALPHA CHAIN PD002608: V164-F288 KINASE PROTEIN TRANSFERASE ATP BINDING SERINE/THREONINE PHOSPHORYLATION RECEPTOR TYROSINE TRANSMEMBRANE PD000001: Y169-P301 PROTEIN KINASE DOMAIN DM00004 P29620 21-289:I10-A279 DM00004 Q00526 6-286:F9-F288 DM00004 P43450 6-276:F9-A279 DM00004 P23437 6-286:F9-F288	HMER_PFAM BLIMPS_PRINTS PROFILESAN MOTIFS MOTIFS BLAST_PRODUM BLAST_PRODUM BLAST_DOMO

Table 4

Poly-nucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment (s)	Sequence Fragments	5' Position	3' Position
19	2890544CB1	4224	1-1378, 4153-4224	6474032H1 (PLACFER01)	545	1204
				71089659V1	2981	3638
				71083920V1	2936	3576
				71083254V1	2263	2853
				71084605V1	2351	2959
				7286979H1 (BRAIFER06)	1	408
				71254276V1	1091	1695
				5980233F7 (MCLDXT02)	3498	4224
				71252928V1	1632	2197
				7086636H1 (BRAUTDR03)	222	702
				71082857V1	1680	2356
				7313223H1 (LIVRFE02)	498	928
20	7472693CB1	1736	72-149, 1337-1736	70520498D1	760	1354
				609792R6 (COLANOT01)	145	736
				61544947	1	385
				70518493D1	716	1182
				70518085D1	1172	1736
21	3107952CB1	1824	1802-1824	7308849H1 (MMLR1DT01)	1215	1807
				2925973F6 (TLYMNOT04)	715	1215
				3459433F6 (293TF1T01)	1	582
				2927552F6 (TLYMNOT04)	1309	1824
				3107952F6 (BRSTTUT15)	507	1161
22	5544420CB1	2201	1285-1629, 2128-2201, 256-376	6922389H1 (PLACFER06)	1458	1597
				7739285H1 (THYMOE01)	646	834
				5544420F6 (TESTNOC01)	807	1187
				4206166F6 (BRONNOT02)	2041	2201
				GNN:95924006_004.edit	368	1871
				GBL:95924006_raw.comp	1	492
				2512558F6 (LIVRUT04)	1617	1720
				92882961	1644	2127
				6909108J1 (PTUDIR01)	1138	1317
23	7472832CB1	2974	2933-2974, 1-654	6910588J1 (PTUDIR01)	1994	2577
				2940460H1 (THYMFET02)	2682	2956
				7274331H2 (KIDETXJ01)	1876	2503
				60205600U1	559	1091

Table 4 (cont.)

Poly-nucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
23				60205598U1	690	1339
				6426807H1 (LUNGNON07)	2411	2951
				3344032H1 (SPLNNOT09)	2708	2958
				6811278J1 (SKIRNOR01)	1	647
				6910588H1 (PITUDIR01)	1369	2003
				91860144	2512	2974
				1732303F6 (BRSTTUT08)	1230	1731
	1551456CB1	3648	1906-2052, 1-752	6830947J1 (SININOR01)	2357	3121
				6834559H1 (BRSTNOR02)	1610	2330
				680891J1 (SKIRNOR01)	222	921
24				1389125H1 (EOSINOT01)	1	246
				1680356F6 (STOMFET01)	3139	3648
				6870264H1 (BRAGNON02)	3374	3648
				7714085J1 (SINTFEE02)	298	950
				7746056H1 (ADRETUE04)	875	1491
				3296183F6 (TLYXJINT01)	1553	2310
				70349297D1	3030	3648
				70872871V1	953	1599
				70875814V1	2218	2955
	2589355CB1	4719	1835-1863, 1-1135, 2380-3186	6500833H1 (PROSTUS25)	2498	3226
				2313925T6 (NGANNOT01)	3264	3885
				6483636F9 (MIXDUNB01)	2716	3270
				70985467V1	388	980
				7251743H1 (PROSTMY01)	810	1299
				6864125H1 (BRAGNON02)	1323	1998
				6056925H1 (BRAENOT04)	1322	1735
				6705826H1 (HEAADIR01)	4080	4719
				7652463H2 (STOMTDE01)	997	1704
25				7039646H1 (UTRSTMR02)	1	566
				7257374H1 (SKIRTDC01)	1977	2560
				70402344D1	3105	3674
				2586850F6 (BRAITUT22)	3840	4348
				924331H1 (RATRNOR02)	4009	4386
	4357117CB1	1651	1-267	GS.4357117.fasta	1	1329
				6131509F6 (BMARTXT02)	1134	1651
26						

Table 4 (cont.)

Poly-nucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
27	5511992CB1	3141	1672-1833, 71-157, 665-828, 1298-1538, 2580-2878	GS.5511992.fasta	1	3141
28	7474560CB1	1244	1205-1244, 1-131	6311370H1 (NERFDN03) 6853555H1 (BRAIFEN08) 6997205H1 (BRAXTDR17)	616 1 691	1236 683 1244
29	7474602CB1	1661	72-149	70518523D1 6772112J1 (BRAUNOR01) 346275T7 (THVMNOT02)	577 1 1043	1171 640 1661
30	7475509CB1	912	881-912	6124350H1 (BRAHNON05) 944796H1 (RATNOT02) 3616204F6 (EPIFN0T01)	634 1 69	1180 93 699
31	7475491CB1	2858	1-269, 2768-2858	71147872V1 7232424H1 (BRAXTDR15) 7004062H1 (COLNFEC01) 7677070J1 (NOSETUE01) 7716833J1 (SINTFEE02) 754239R6 (BRAITUT02) 7067423H1 (BRATNOR01) 7428450H1 (UTRMTMR02) 70680595V1	1831 1967 1 1293 1000 499 2179 654	2429 2495 564 1877 1575 1106 2858 1111
32	2192119CB1	2817	1-249	1687835F6 (PROSTUT10) 6769461J1 (BRAUNOR01) 1819105F6 (PROSN0T20) 7716523H1 (SINTFEE02) 1796441T6 (PROSTUT05) 1618475T6 (BRAITUT12) 7675143H1 (NOSETUE01) 6145288H1 (BRANDIT03) 3189653H1 (THYMNON04) 7646563H1 (UTRSTUE01) 96700560	2416 221 1052 498 2186 2117 1130 1543 1855 367 1	2817 385 1721 1072 2793 2783 1739 2170 2196 1049 393
33	7474496CB1	5305	3463-3753, 1403-1781, 2384-2464, 1-644, 5126-5305	70886570V1	3332	3875

Table 4 (cont.)

Poly-nucleotide SEQ ID NO.	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
33				429360R6 (BLADNOT01)	2735	3311
				70885734V1	4100	4744
				1830377F6 (THP1AZT01)	3649	4093
				6488464H1 (MIXDUNB01)	2852	3473
				488190R6 (HNT2ACT01)	2317	2865
				70888476V1	4651	5305
				1832566R6 (BRAINON01)	4034	4547
34	1834248CB1	3269	1754-1773, 1-142, 3072-3269	GNN.G7139831_000025_004	1293	2275
				6146293H1 (BRANDIT03)	1791	2354
				6272238H2 (BRAIFEN03)	2635	3263
				6893004J1 (BRAITDR03)	684	1248
				7663341J1 (UTRSTME01)	873	1492
				4001427R6 (HNT2AZS07)	2927	3264
				60202068B1	2368	2916
				60202069B1	2334	2864
				6954283H1 (BRAITDR02)	1	718
				9810284	2771	3269
	71584520CB1	3017	2968-3017, 1-49, 1234-1322, 679-736	1287320T6 (BRAINOT11)	2615	2983
				71579751V1	1083	1791
				71580777V1	586	1149
				6764749H1 (BRAUNOR01)	1406	2001
35				7581090H1 (BRAIFEC01)	1	577
				1295833H1 (PGANNO03)	2783	3017
				1414795F6 (BRAINOT12)	2183	2508
				7362189H1 (BRAIFER05)	458	1003
				2157112T6 (BRAINOT09)	2388	2977
				2157112F6 (BRAINOT09)	1963	2450
	7475538CB1	2168	811-870, 933-1227	6855691H1 (BRAIFEN08)	1500	2168
				70644867V1	613	1261
				70645804V1	515	1249
				70645323V1	1	595
36				71564044V1	1277	1993
				71565564V1	1156	1924

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
19	2890544CB1	MCLDXT02
20	7472693CB1	COLNNOT01
21	3107952CB1	TLYMN0T04
22	5544420CB1	SEMVN0T01
23	7472832CB1	SKIRN0R01
24	1551456CB1	LVENNOT03
25	2589355CB1	BRADDIR01
26	4357117CB1	EMARTXT02
27	5511992CB1	SINTFEE02
28	7474560CB1	BRAYDIN03
29	7474602CB1	COLNNOT01
30	7475509CB1	BRATVUT21
31	7475491CB1	SCOMDIT01
32	2192119CB1	PROSTUS23
33	7474496CB1	BRAINON01
34	1834248CB1	BRATVUT22
35	71584520CB1	BRAIFEC01
36	7475538CB1	BRAIFEN08

Table 6

Library	Vector	Library Description
BWARTXT02	pINCY	Library was constructed using RNA isolated from treated SH-SY5Y cell line derived from bone marrow neuroblastoma tumor cells removed from a 4-year-old Caucasian female. The cells were cultured in the presence of retinoic acid.
BRADDIR01	pINCY	Library was constructed using RNA isolated from diseased choroid plexus tissue of the lateral ventricle, removed from the brain of a 57-year-old Caucasian male, who died from a cerebrovascular accident.
BRAIFEC01	pINCY	This large size-fractionated library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus who was stillborn with a hypoplastic left heart at 23 weeks' gestation.
BRAIFEN08	pINCY	This normalized fetal brain tissue library was constructed from 400 thousand independent clones from a fetal brain tissue library. Starting RNA was made from brain tissue removed from a Caucasian male fetus who was stillborn with a hypoplastic left heart at 23 weeks' gestation. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48 hours/round) reannealing hybridization was used.
BRAINON01	PSPORT1	Library was constructed and normalized from 4.88 million independent clones from a brain tissue library. RNA was made from brain tissue removed from a 26-year-old Caucasian male during cranioplasty and excision of a cerebral meningeal lesion. Pathology for the associated tumor tissue indicated a grade 4 oligoastrocytoma in the right fronto-parietal part of the brain.
BRAITUT21	pINCY	Library was constructed using RNA isolated from brain tumor tissue removed from the midline frontal lobe of a 61-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated subfrontal meningothelial meningioma with no atypia. One ethmoid and mucosal tissue sample indicated meningioma. Family history included cerebrovascular disease, senile dementia, hyperlipidemia, benign hypertension, atherosclerotic coronary artery disease, congestive heart failure, and breast cancer.
BRAITUT22	pINCY	Library was constructed using RNA isolated from brain tumor tissue removed from the right frontal/parietal lobe of a 76-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated a meningioma. Family history included senile dementia.

Table 6 (cont.)

Library	Vector	Library Description
BRAYDIN03	pINCY	This normalized brain tissue library was constructed from 6.7 million independent clones from the BRAYDIT01 tissue library. Starting RNA was made from RNA isolated from diseased hypothalamus tissue removed from a 57-year-old Caucasian male who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91:9228 and Bonaldo et al., Genome Research (1996) 6:791, except that a significantly longer (48 -hours/round) reannealing hybridization was used. The library was linearized and recircularized to select for insert containing clones.
COLNNOT01	PSPORT1	Library was constructed using RNA isolated from colon tissue removed from a 75-year-old Caucasian male during a hemicolectomy.
LVENNOT03	PSPORT1	Library was constructed using RNA isolated from the left ventricle tissue of a 31-year-old male.
MCLDXT02	pINCY	Library was constructed using RNA isolated from treated umbilical cord blood dendritic cells removed from a male. The cells were treated with granulocyte/macrophage colony stimulating factor (GM-CSF), tumor necrosis factor alpha (TNF alpha), stem cell factor (SCF), phorbol myristate acetate (PMA), and ionomycin. The GM-CSF was added at time 0 at 100 ng/ml, the TNF alpha was added at time 0 at 2.5 ng/ml, the SCF was added at time 0 at 25 ng/ml. The PMA and ionomycin were added at 13 days for five hours. Incubation time was 13 days.

Table 6 (cont.)

Library	Vector	Library Description
PROSTUS23	pINCY	This subtracted prostate tumor library was constructed using 10 million clones from a pooled prostate tumor library that was subjected to 2 rounds of subtractive hybridization with 10 million clones from a pooled prostate tissue library. The starting library for subtraction was constructed by pooling equal numbers of clones from 4 prostate tumor libraries using mRNA isolated from prostate tumor removed from Caucasian males at ages 58 (A), 61 (B), 66 (C), and 68 (D) during prostatectomy with lymph node excision. Pathology indicated adenocarcinoma in all donors. History included elevated PSA, induration and tobacco abuse in donor A; elevated PSA, induration, prostate hyperplasia, renal failure, osteoarthritis, renal artery stenosis, benign HTN, thrombocytopenia, hyperlipidemia, tobacco/alcohol abuse and hepatitis C (carrier) in donor B; elevated PSA, induration, and tobacco abuse in donor C; and elevated PSA, induration, hypercholesterolemia, and kidney calculus in donor D. The hybridization probe for subtraction was constructed by pooling equal numbers of cDNA clones from 3 prostate tissue libraries derived from prostate tissue, prostate epithelial cells, and fibroblasts from prostate stroma from 3 different donors. Subtractive hybridization conditions were based on the methodologies of Swaroop et al., NAR 19 (1991):1954 and Bonaldo, et al. Genome Research 6 (1996):791.
SCOMDIT01	pINCY	Library was constructed using RNA isolated from diseased spinal cord tissue removed from the base of the medulla of a 57-year-old Caucasian male who died from a cerebrovascular accident. Patient history included Huntington's disease and emphysema.
SEMVMOT01	pINCY	Library was constructed using RNA isolated from seminal vesicle tissue removed from a 58-year-old Caucasian male during radical prostatectomy. Pathology for the associated tumor tissue indicated adenocarcinoma (Gleason grade 3+2) of the prostate. Adenofibromatous hyperplasia was also present. The patient presented with elevated prostate specific antigen (PSA). Family history included a malignant breast neoplasm.
SINTFEE02	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from small intestine tissue removed from a Caucasian male fetus who died from Patau's syndrome (trisomy 13) at 20-weeks' gestation. Serology was negative.
SKIRNOR01	PCDNA2.1	This random primed library was constructed using RNA isolated from skin tissue removed from the breast of a 17-year-old Caucasian female during bilateral reduction mammaplasty. Patient history included breast hypertrophy. Family history included benign hypertension.
TYMNOT04	pINCY	Library was constructed using RNA isolated from activated Th1 cells. These cells were differentiated from umbilical cord CD4 T cells with IL-12 and B7-transfected COS cells, and then activated for six hours with anti-CD3 and anti-CD28 antibodies.

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.0E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1998) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less Signal peptide hits: Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of
5 SEQ ID NO:1-18,
 - b) a naturally occurring polypeptide comprising an amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:2-18,
 - c) a naturally occurring polypeptide comprising an amino acid sequence at least 98% identical to an amino acid sequence of SEQ ID NO:1,
 - 10 d) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, and
 - e) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18.
- 15 2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-18.
3. An isolated polynucleotide encoding a polypeptide of claim 1.
- 20 4. An isolated polynucleotide encoding a polypeptide of claim 2.
5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:19-36.
- 25 6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
7. A cell transformed with a recombinant polynucleotide of claim 6.
- 30 8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
9. A method for producing a polypeptide of claim 1, the method comprising:
 - a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide

comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and

b) recovering the polypeptide so expressed.

5 10. An isolated antibody which specifically binds to a polypeptide of claim 1.

11. An isolated polynucleotide selected from the group consisting of:

a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:19-36,

10 b) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:20-36,

c) a naturally occurring polynucleotide comprising a polynucleotide sequence at least 98% identical to the polynucleotide sequence of SEQ ID NO:19,

d) a polynucleotide complementary to a polynucleotide of a),

15 e) a polynucleotide complementary to a polynucleotide of b),

f) a polynucleotide complementary to a polynucleotide of c), and

g) an RNA equivalent of a)-f).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a
20 polynucleotide of claim 11.

13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides
25 comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and

b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

30

14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and

b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

5

16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected
10 from the group consisting of SEQ ID NO:1-18.

18. A method for treating a disease or condition associated with decreased expression of functional PKIN, comprising administering to a patient in need of such treatment the composition of claim 16.

15

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

20

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of
25 functional PKIN, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

30

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

24. A method for treating a disease or condition associated with overexpression of functional PKIN, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim 1, said method comprising the steps of:

- a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and
- b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

28. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological

sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;

- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

29. A diagnostic test for a condition or disease associated with the expression of PKIN in a biological sample comprising the steps of:

- a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and
- b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

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30. The antibody of claim 10, wherein the antibody is:

- a) a chimeric antibody,
- b) a single chain antibody,
- c) a Fab fragment,
- d) a F(ab')₂ fragment, or
- e) a humanized antibody.

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31. A composition comprising an antibody of claim 10 and an acceptable excipient.

32. A method of diagnosing a condition or disease associated with the expression of PKIN in a subject, comprising administering to said subject an effective amount of the composition of claim 31.

33. A composition of claim 31, wherein the antibody is labeled.

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34. A method of diagnosing a condition or disease associated with the expression of PKIN in a subject, comprising administering to said subject an effective amount of the composition of claim 33.

35. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 10 comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, or an immunogenic fragment thereof, under conditions to elicit an antibody response;
- b) isolating antibodies from said animal; and
- c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18.

36. An antibody produced by a method of claim 35.

37. A composition comprising the antibody of claim 36 and a suitable carrier.

38. A method of making a monoclonal antibody with the specificity of the antibody of claim 10 comprising:

- a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18, or an immunogenic fragment thereof, under conditions to elicit an antibody response;
- b) isolating antibody producing cells from the animal;
- c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells;
- d) culturing the hybridoma cells; and
- e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18.

39. A monoclonal antibody produced by a method of claim 38.

40. A composition comprising the antibody of claim 39 and a suitable carrier.

41. The antibody of claim 10, wherein the antibody is produced by screening a Fab expression library.

42. The antibody of claim 10, wherein the antibody is produced by screening a recombinant

immunoglobulin library.

43. A method for detecting a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18 in a sample, comprising the steps of:

- 5 a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and
- b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18 in the sample.

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44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18 from a sample, the method comprising:

- a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and
- 15 b) separating the antibody from the sample and obtaining the purified polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-18.

45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

20 46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

25

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

30

51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.
55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.
56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.
57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.
58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.
59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.
60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.
61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.
62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.
63. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:19.
64. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:20.
65. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:21.
66. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:22.
67. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:23.

68. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:24.

69. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:25.

70. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:26.

71. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:27.

72. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:28.

73. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:29.

74. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:30.

75. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:31.

76. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:32.

77. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:33.

78. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:34.

79. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID

NO:35.

80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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Phe Ala Lys Ser Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val
305 310 315
Val Arg His Met Arg Lys Leu His Leu Gly Ser Ser Leu Asp Ser
320 325 330
Ser Asn Ala Ser Val Ser Ser Ser Leu Ser Leu Ala Ser Gln Lys
335 340 345
Asp Cys Ala Tyr Val Ala Lys Pro Glu Ser Leu Ser
350 355

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<210> 3

<211> 419

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3107952CD1

<400> 3

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Met Ala Gly Ser Gly Cys Ala Trp Gly Ala Glu Pro Pro Arg Phe
1 5 10 15
Leu Glu Ala Phe Gly Arg Leu Trp Gln Val Gln Ser Arg Leu Gly
20 25 30
Ser Gly Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys Gly Asn
35 40 45
Pro Gly Ser Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro Gly
50 55 60
Thr Thr Gly Ala Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys
65 70 75
Glu Arg Ala Ala Leu Glu Gln Leu Gln Gly His Arg Asn Ile Val
80 85 90
Thr Leu Tyr Gly Val Phe Thr Ile His Phe Ser Pro Asn Val Pro
95 100 105
Ser Arg Cys Leu Leu Leu Glu Leu Leu Asp Val Ser Val Ser Glu
110 115 120
Leu Leu Leu Tyr Ser Ser His Gln Gly Cys Ser Met Trp Met Ile
125 130 135
Gln His Cys Ala Arg Asp Val Leu Glu Ala Leu Ala Phe Leu His
140 145 150
His Glu Gly Tyr Val His Ala Asp Leu Lys Pro Arg Asn Ile Leu
155 160 165
Trp Ser Ala Glu Asn Glu Cys Phe Lys Leu Ile Asp Phe Gly Leu
170 175 180

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Ser	Phe	Lys	Glu	Gly	Asn	Gln	Asp	Val	Lys	Tyr	Ile	Gln	Thr	Asp	185	190	195
Gly	Tyr	Arg	Ala	Pro	Glu	Ala	Glu	Leu	Gln	Asn	Cys	Leu	Ala	Gln	200	205	210
Ala	Gly	Leu	Gln	Ser	Asp	Thr	Glu	Cys	Thr	Ser	Ala	Val	Asp	Leu	215	220	225
Trp	Ser	Leu	Gly	Ile	Ile	Leu	Leu	Glu	Met	Phe	Ser	Gly	Met	Lys	230	235	240
Leu	Lys	His	Thr	Val	Arg	Ser	Gln	Glu	Trp	Lys	Ala	Asn	Ser	Ser	245	250	255
Ala	Ile	Ile	Asp	His	Ile	Phe	Ala	Ser	Lys	Ala	Val	Val	Asn	Ala	260	265	270
Ala	Ile	Pro	Ala	Tyr	His	Leu	Arg	Asp	Leu	Ile	Lys	Ser	Met	Leu	275	280	285
His	Asp	Asp	Pro	Ser	Arg	Arg	Ile	Pro	Ala	Glu	Met	Ala	Leu	Cys	290	295	300
Ser	Pro	Phe	Phe	Ser	Ile	Pro	Phe	Ala	Pro	His	Ile	Glu	Asp	Leu	305	310	315
Val	Met	Leu	Pro	Thr	Pro	Val	Leu	Arg	Leu	Leu	Asn	Val	Leu	Asp	320	325	330
Asp	Asp	Tyr	Leu	Glu	Asn	Glu	Glu	Glu	Tyr	Glu	Asp	Val	Val	Glu	335	340	345
Asp	Val	Lys	Glu	Glu	Cys	Gln	Lys	Tyr	Gly	Pro	Val	Val	Ser	Leu	350	355	360
Leu	Val	Pro	Lys	Gly	Asn	Pro	Gly	Arg	Gly	Gln	Val	Phe	Val	Glu	365	370	375
Tyr	Ala	Asn	Ala	Gly	Asp	Ser	Lys	Ala	Ala	Gln	Lys	Leu	Leu	Thr	380	385	390
Gly	Arg	Met	Phe	Asp	Gly	Lys	Phe	Val	Val	Ala	Thr	Phe	Tyr	Pro	395	400	405
Leu	Ser	Ala	Tyr	Lys	Arg	Gly	Tyr	Leu	Tyr	Gln	Thr	Leu	Leu		410	415	

<210> 4

<211> 624

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5544420CD1

<400> 4

Met	Asn	Arg	Tyr	Thr	Thr	Met	Arg	Gln	Leu	Gly	Asp	Gly	Thr	Tyr	1	5	10	15
Gly	Ser	Val	Leu	Met	Gly	Lys	Ser	Asn	Glu	Ser	Gly	Glu	Leu	Val	20	25	30	
Ala	Ile	Lys	Arg	Met	Lys	Arg	Lys	Phe	Tyr	Ser	Trp	Asp	Glu	Cys	35	40	45	
Met	Asn	Leu	Arg	Glu	Val	Lys	Ser	Leu	Lys	Lys	Leu	Asn	His	Ala	50	55	60	
Asn	Val	Ile	Lys	Leu	Lys	Glu	Val	Ile	Arg	Glu	Asn	Asp	His	Leu	65	70	75	
Tyr	Phe	Ile	Phe	Glu	Tyr	Met	Lys	Glu	Asn	Leu	Tyr	Gln	Leu	Met	80	85	90	
Lys	Asp	Arg	Asn	Lys	Leu	Phe	Pro	Glu	Ser	Val	Ile	Arg	Asn	Ile	95	100	105	
Met	Tyr	Gln	Ile	Leu	Gln	Gly	Leu	Ala	Phe	Ile	His	Lys	His	Gly	110	115	120	
Phe	Phe	His	Arg	Asp	Met	Lys	Pro	Glu	Asn	Leu	Leu	Cys	Met	Gly	125	130	135	
Pro	Glu	Leu	Val	Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Glu	Leu	140	145	150	

Arg Ser Gln Pro	Pro Tyr Thr Asp Tyr	Val Ser Thr Arg Trp	Tyr
	155	160	165
Arg Ala Pro Glu	Val Leu Leu Arg Ser	Ser Val Tyr Ser Ser	Pro
	170	175	180
Ile Asp Val Trp	Ala Val Gly Ser Ile	Met Ala Glu Leu Tyr	Met
	185	190	195
Leu Arg Pro Leu	Phe Pro Gly Thr Ser	Glu Val Asp Glu Ile	Phe
	200	205	210
Lys Ile Cys Gln	Val Leu Gly Thr Pro	Lys Lys Ser Asp Trp	Pro
	215	220	225
Glu Gly Tyr Gln	Leu Ala Ser Ser Met	Asn Phe Arg Phe Pro	Gln
	230	235	240
Cys Val Pro Ile	Asn Leu Lys Thr Leu	Ile Pro Asn Ala Ser	Asn
	245	250	255
Glu Ala Ile Gln	Leu Met Thr Glu Met	Leu Asn Trp Asp Pro	Lys
	260	265	270
Lys Arg Pro Thr	Ala Ser Gln Ala Leu	Lys His Pro Tyr Phe	Gln
	275	280	285
Val Gly Gln Val	Leu Gly Pro Ser Ser	Asn His Leu Glu Ser	Lys
	290	295	300
Gln Ser Leu Asn	Lys Gln Leu Gln Pro	Leu Glu Ser Lys Pro	Ser
	305	310	315
Leu Val Glu Val	Glu Pro Lys Pro Leu	Pro Asp Ile Ile Asp	Gln
	320	325	330
Val Val Gly Gln	Pro Gln Pro Lys Thr	Ser Gln Gln Pro Leu	Gln
	335	340	345
Pro Ile Gln Pro	Pro Gln Asn Leu Ser	Val Gln Gln Pro Pro	Lys
	350	355	360
Gln Gln Ser Gln	Glu Lys Pro Pro Gln	Thr Leu Phe Pro Ser	Ile
	365	370	375
Val Lys Asn Met	Pro Thr Lys Pro Asn	Gly Thr Leu Ser His	Lys
	380	385	390
Ser Gly Arg Arg	Arg Trp Gly Gln Thr	Ile Phe Lys Ser Gly	Asp
	395	400	405
Ser Trp Glu Glu	Leu Glu Asp Tyr Asp	Phe Gly Ala Ser His	Ser
	410	415	420
Lys Lys Pro Ser	Met Gly Val Phe Lys	Glu Lys Arg Lys Lys	Asp
	425	430	435
Ser Pro Phe Arg	Leu Pro Glu Pro Val	Pro Ser Gly Ser Asn	His
	440	445	450
Ser Thr Gly Glu	Asn Lys Ser Leu Pro	Ala Val Thr Ser Leu	Lys
	455	460	465
Ser Asp Ser Glu	Leu Ser Thr Ala Pro	Thr Ser Lys Gln Tyr	Tyr
	470	475	480
Leu Lys Gln Ser	Arg Tyr Leu Pro Gly	Val Asn Pro Lys Lys	Val
	485	490	495
Ser Leu Ile Ala	Ser Gly Lys Glu Ile	Asn Pro His Thr Trp	Ser
	500	505	510
Asn Gln Leu Phe	Pro Lys Ser Leu Gly	Pro Val Gly Ala Glu	Leu
	515	520	525
Ala Phe Lys Arg	Ser Asn Ala Glu Glu	Lys Leu Gly Ser Tyr	Ala
	530	535	540
Thr Tyr Asn Gln	Ser Gly Tyr Ile Pro	Ser Phe Leu Lys Lys	Glu
	545	550	555
Val Gln Ser Ala	Gly Gln Arg Ile His	Leu Ala Pro Leu Asn	Ala
	560	565	570
Thr Ala Ser Glu	Tyr Thr Trp Asn Thr	Lys Thr Gly Arg Gly	Gln
	575	580	585
Phe Ser Gly Arg	Thr Tyr Asn Pro Thr	Ala Lys Asn Leu Asn	Ile
	590	595	600
Val Asn Arg Ala	Gln Pro Ile Pro Ser	Val His Gly Arg Thr	Asp
	605	610	615
Trp Val Ala Lys	Tyr Gly Gly His Arg		

620

<210> 5
 <211> 878
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7472832CD1

<400> 5
 Met Ala Thr Ala Pro Ser Tyr Pro Ala Gly Leu Pro Gly Ser Pro
 1 5 10 15
 Gly Pro Gly Ser Pro Pro Pro Pro Gly Gly Leu Glu Leu Gln Ser
 20 25 30
 Pro Pro Pro Leu Leu Pro Gln Ile Pro Ala Pro Gly Ser Gly Val
 35 40 45
 Ser Phe His Ile Gln Ile Gly Leu Thr Arg Glu Phe Val Leu Leu
 50 55 60
 Pro Ala Ala Ser Glu Leu Ala His Val Lys Gln Leu Ala Cys Ser
 65 70 75
 Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly Leu Tyr
 80 85 90
 Asp Lys Ile Leu Leu Phe Lys His Asp Pro Thr Ser Ala Asn Leu
 95 100 105
 Leu Gln Leu Val Arg Ser Ser Gly Asp Ile Gln Glu Gly Asp Leu
 110 115 120
 Val Glu Val Val Leu Ser Ala Ser Ala Thr Phe Glu Asp Phe Gln
 125 130 135
 Ile Arg Pro His Ala Leu Thr Val His Ser Tyr Arg Ala Pro Ala
 140 145 150
 Phe Cys Asp His Cys Gly Glu Met Leu Phe Gly Leu Val Arg Gln
 155 160 165
 Gly Leu Lys Cys Asp Gly Cys Gly Leu Asn Tyr His Lys Arg Cys
 170 175 180
 Ala Phe Ser Ile Pro Asn Asn Cys Ser Gly Ala Arg Lys Arg Arg
 185 190 195
 Leu Ser Ser Thr Ser Leu Ala Ser Gly His Ser Val Arg Leu Gly
 200 205 210
 Thr Ser Glu Ser Leu Pro Cys Thr Ala Glu Glu Leu Ser Arg Ser
 215 220 225
 Thr Thr Glu Leu Leu Pro Arg Arg Pro Pro Ser Ser Ser Ser Ser
 230 235 240
 Ser Ser Ala Ser Ser Tyr Thr Gly Arg Pro Ile Glu Leu Asp Lys
 245 250 255
 Met Leu Leu Ser Lys Val Lys Val Pro His Thr Phe Leu Ile His
 260 265 270
 Ser Tyr Thr Arg Pro Thr Val Cys Gln Ala Cys Lys Lys Leu Leu
 275 280 285
 Lys Gly Leu Phe Arg Gln Gly Leu Gln Cys Lys Asp Cys Lys Phe
 290 295 300
 Asn Cys His Lys Arg Cys Ala Thr Arg Val Pro Asn Asp Cys Leu
 305 310 315
 Gly Glu Ala Leu Ile Asn Gly Asp Val Pro Met Glu Glu Ala Thr
 320 325 330
 Asp Phe Ser Glu Ala Asp Lys Ser Ala Leu Met Asp Glu Ser Glu
 335 340 345
 Asp Ser Gly Val Ile Pro Gly Ser His Ser Glu Asn Ala Leu His
 350 355 360
 Ala Ser Glu Glu Glu Gly Glu Gly Gly Lys Ala Gln Ser Ser
 365 370 375
 Leu Gly Tyr Ile Pro Leu Met Arg Val Val Gln Ser Val Arg His

	380		385		390
Thr Thr Arg Lys	Ser Ser Thr Thr Leu	Arg Glu Gly Trp Val	Val		
	395		400		405
His Tyr Ser Asn	Lys Asp Thr Leu Arg	Lys Arg His Tyr Trp	Arg		
	410		415		420
Leu Asp Cys Lys	Cys Ile Thr Leu Phe	Gln Asn Asn Thr Thr	Asn		
	425		430		435
Arg Tyr Tyr Lys	Glu Ile Pro Leu Ser	Glu Ile Leu Thr Val	Glu		
	440		445		450
Ser Ala Gln Asn	Phe Ser Leu Val Pro	Pro Gly Thr Asn Pro	His		
	455		460		465
Cys Phe Glu Ile	Val Thr Ala Asn Ala	Thr Tyr Phe Val Gly	Glu		
	470		475		480
Met Pro Gly Gly	Thr Pro Gly Gly Pro	Ser Gly Gln Gly Ala	Glu		
	485		490		495
Ala Ala Arg Gly	Trp Glu Thr Ala Ile	Arg Gln Ala Leu Met	Pro		
	500		505		510
Val Ile Leu Gln	Asp Ala Pro Ser Ala	Pro Gly His Ala Pro	His		
	515		520		525
Arg Gln Ala Ser	Leu Ser Ile Ser Val	Ser Asn Ser Gln Ile	Gln		
	530		535		540
Glu Asn Val Asp	Ile Ala Thr Val Tyr	Gln Ile Phe Pro Asp	Glu		
	545		550		555
Val Leu Gly Ser	Gly Gln Phe Gly Val	Val Tyr Gly Gly Lys	His		
	560		565		570
Arg Lys Thr Gly	Arg Asp Val Ala Val	Lys Val Ile Asp Lys	Leu		
	575		580		585
Arg Phe Pro Thr	Lys Gln Glu Ser Gln	Leu Arg Asn Glu Val	Ala		
	590		595		600
Ile Leu Gln Ser	Leu Arg His Pro Gly	Ile Val Asn Leu Glu	Cys		
	605		610		615
Met Phe Glu Thr	Pro Glu Lys Val Phe	Val Val Met Glu Lys	Leu		
	620		625		630
His Gly Asp Met	Leu Glu Met Ile Leu	Ser Ser Glu Lys Gly	Arg		
	635		640		645
Leu Pro Glu Arg	Leu Thr Lys Phe Leu	Ile Thr Gln Ile Leu	Val		
	650		655		660
Ala Leu Arg His	Leu His Phe Lys Asn	Ile Val His Cys Asp	Leu		
	665		670		675
Lys Pro Glu Asn	Val Leu Leu Ala Ser	Ala Asp Pro Phe Pro	Gln		
	680		685		690
Val Lys Leu Cys	Asp Phe Gly Phe Ala	Arg Ile Ile Gly Glu	Lys		
	695		700		705
Ser Phe Arg Arg	Ser Val Val Gly Thr	Pro Ala Tyr Leu Ala	Pro		
	710		715		720
Glu Val Leu Leu	Asn Gln Gly Tyr Asn	Arg Ser Leu Asp Met	Trp		
	725		730		735
Ser Val Gly Val	Ile Met Tyr Val Ser	Leu Ser Gly Thr Phe	Pro		
	740		745		750
Phe Asn Glu Asp	Glu Asp Ile Asn Asp	Gln Ile Gln Asn Ala	Ala		
	755		760		765
Phe Met Tyr Pro	Ala Ser Pro Trp Ser	His Ile Ser Ala Gly	Ala		
	770		775		780
Ile Asp Leu Ile	Asn Asn Leu Leu Gln	Val Lys Met Arg Lys	Arg		
	785		790		795
Tyr Ser Val Asp	Lys Ser Leu Ser His	Pro Trp Leu Gln Glu	Tyr		
	800		805		810
Gln Thr Trp Leu	Asp Leu Arg Glu Leu	Glu Gly Lys Met Gly	Glu		
	815		820		825
Arg Tyr Ile Thr	His Glu Ser Asp Asp	Ala Arg Trp Glu Gln	Phe		
	830		835		840
Ala Ala Glu His	Pro Leu Pro Gly Ser	Gly Leu Pro Thr Asp	Arg		
	845		850		855

Asp Leu Gly Gly Ala Cys Pro Pro Gln Asp His Asp Met Gln Gly
 860 865 870
 Leu Ala Glu Arg Ile Ser Val Leu
 875

<210> 6
 <211> 440
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1551456CD1

<400> 6
 Met Ser Lys Leu Arg Met Lys Arg Arg Ala Ser Asp Arg Gly Ala
 1 5 10 15
 Gly Glu Thr Ser Ala Arg Ala Lys Ala Leu Gly Ser Gly Ile Ser
 20 25 30
 Gly Asn Asn Ala Lys Arg Ala Gly Pro Phe Ile Leu Gly Pro Arg
 35 40 45
 Leu Gly Asn Ser Pro Val Pro Ser Ile Val Gln Cys Leu Ala Arg
 50 55 60
 Lys Asp Gly Thr Asp Asp Phe Tyr Gln Leu Lys Ile Leu Thr Leu
 65 70 75
 Glu Glu Arg Gly Asp Gln Gly Ile Glu Ser Gln Glu Glu Arg Gln
 80 85 90
 Gly Lys Met Leu Leu His Thr Glu Tyr Ser Leu Leu Ser Leu Leu
 95 100 105
 His Thr Gln Asp Gly Val Val His His His Gly Leu Phe Gln Asp
 110 115 120
 Arg Thr Cys Glu Ile Val Glu Asp Thr Glu Ser Ser Arg Met Val
 125 130 135
 Lys Lys Met Lys Lys Arg Ile Cys Leu Val Leu Asp Cys Leu Cys
 140 145 150
 Ala His Asp Phe Ser Asp Lys Thr Ala Asp Leu Ile Asn Leu Gln
 155 160 165
 His Tyr Val Ile Lys Glu Lys Arg Leu Ser Glu Arg Glu Thr Val
 170 175 180
 Val Ile Phe Tyr Asp Val Val Arg Val Val Glu Ala Leu His Gln
 185 190 195
 Lys Asn Ile Val His Arg Asp Leu Lys Leu Gly Asn Met Val Leu
 200 205 210
 Asn Lys Arg Thr His Arg Ile Thr Ile Thr Asn Phe Cys Leu Gly
 215 220 225
 Lys His Leu Val Ser Glu Gly Asp Leu Leu Lys Asp Gln Arg Gly
 230 235 240
 Ser Pro Ala Tyr Ile Ser Pro Asp Val Leu Ser Gly Arg Pro Tyr
 245 250 255
 Arg Gly Lys Pro Ser Asp Met Trp Ala Leu Gly Val Val Leu Phe
 260 265 270
 Thr Met Leu Tyr Gly Gln Phe Pro Phe Tyr Asp Ser Ile Pro Gln
 275 280 285
 Glu Leu Phe Arg Lys Ile Lys Ala Ala Glu Tyr Thr Ile Pro Glu
 290 295 300
 Asp Gly Arg Val Ser Glu Asn Thr Val Cys Leu Ile Arg Lys Leu
 305 310 315
 Leu Val Leu Asp Pro Gln Gln Arg Leu Ala Ala Ala Asp Val Leu
 320 325 330
 Glu Ala Leu Ser Ala Ile Ile Ala Ser Trp Gln Ser Leu Ser Ser
 335 340 345
 Leu Ser Gly Pro Leu Gln Val Val Pro Asp Ile Asp Asp Gln Met
 350 355 360

Ser Asn Ala Asp	Ser Ser Gln Glu Ala	Lys Val Thr Glu Glu Cys	
365		370	375
Ser Gln Tyr Glu	Phe Glu Asn Tyr Met	Arg Gln Gln Leu Leu Leu	
380		385	390
Ala Glu Glu Lys	Ser Ser Ile His Asp	Ala Arg Ser Trp Val Pro	
395		400	405
Lys Arg Gln Phe	Gly Ser Ala Pro Pro	Val Arg Arg Leu Gly His	
410		415	420
Asp Ala Gln Pro	Met Thr Ser Leu Asp	Thr Ala Ile Leu Ala Gln	
425		430	435
Arg Tyr Leu Arg	Lys		
440			

<210> 7

<211> 923

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2589355CD1

<400> 7

Met Ala Arg Gly Thr Cys Ser Ala Gly Arg Ser Gly Trp Gly Ser	
1 5 10 15	
Thr Thr Ser Arg Ala Arg Trp Ala Ser Gly Asn Phe Ala Val Val	
20 25 30	
Lys Leu Gly Arg His Arg Ile Thr Lys Thr Glu Val Ala Ile Lys	
35 40 45	
Ile Ile Asp Lys Ser Gln Pro Trp Met His Val Asn Leu Glu Lys	
50 55 60	
Ile Tyr Arg Glu Val Gln Ile Met Lys Met Leu Asp His Pro His	
65 70 75	
Ile Ile Lys Leu Tyr Gln Val Met Glu Thr Lys Ser Met Leu Tyr	
80 85 90	
Leu Val Thr Glu Tyr Ala Lys Asn Gly Glu Ile Phe Asp Tyr Leu	
95 100 105	
Ala Asn His Gly Arg Leu Asn Glu Ser Glu Ala Arg Arg Lys Phe	
110 115 120	
Trp Gln Ile Leu Ser Ala Val Asp Tyr Cys His Gly Arg Lys Ile	
125 130 135	
Val His Arg Asp Leu Lys Ala Glu Asn Leu Leu Leu Asp Asn Asn	
140 145 150	
Met Asn Ile Lys Ile Ala Asp Phe Gly Phe Gly Asn Phe Phe Lys	
155 160 165	
Ser Gly Glu Leu Leu Ala Thr Trp Cys Gly Ser Pro Pro Tyr Ala	
170 175 180	
Ala Pro Glu Val Phe Glu Gly Gln Gln Tyr Glu Gly Pro Gln Leu	
185 190 195	
Asp Ile Trp Ser Met Gly Val Val Leu Tyr Val Leu Val Cys Gly	
200 205 210	
Ala Leu Pro Phe Asp Gly Pro Thr Leu Pro Ile Leu Arg Gln Arg	
215 220 225	
Val Leu Glu Gly Arg Phe Arg Ile Pro Tyr Phe Met Ser Glu Asp	
230 235 240	
Cys Glu His Leu Ile Arg Arg Met Leu Val Leu Asp Pro Ser Lys	
245 250 255	
Arg Leu Thr Ile Ala Gln Ile Lys Glu His Lys Trp Met Leu Ile	
260 265 270	
Glu Val Pro Val Gln Arg Pro Val Leu Tyr Pro Gln Glu Gln Glu	
275 280 285	
Asn Glu Pro Ser Ile Gly Glu Phe Asn Glu Gln Val Leu Arg Leu	
290 295 300	

Met	His	Ser	Leu	Gly	Ile	Asp	Gln	Gln	Lys	Thr	Ile	Glu	Ser	Leu
				305					310					315
Gln	Asn	Lys	Ser	Tyr	Asn	His	Phe	Ala	Ala	Ile	Tyr	Phe	Leu	Leu
				320					325					330
Val	Glu	Arg	Leu	Lys	Ser	His	Arg	Ser	Ser	Phe	Pro	Val	Glu	Gln
				335					340					345
Arg	Leu	Asp	Gly	Arg	Gln	Arg	Arg	Pro	Ser	Thr	Ile	Ala	Glu	Gln
				350					355					360
Thr	Val	Ala	Lys	Ala	Gln	Thr	Val	Gly	Leu	Pro	Val	Thr	Met	His
				365					370					375
Ser	Pro	Asn	Met	Arg	Leu	Leu	Arg	Ser	Ala	Leu	Leu	Pro	Gln	Ala
				380					385					390
Ser	Asn	Val	Glu	Ala	Phe	Ser	Phe	Pro	Ala	Ser	Gly	Cys	Gln	Ala
				395					400					405
Glu	Ala	Ala	Phe	Met	Glu	Glu	Glu	Cys	Val	Asp	Thr	Pro	Lys	Val
				410					415					420
Asn	Gly	Cys	Leu	Leu	Asp	Pro	Val	Pro	Pro	Val	Leu	Val	Arg	Lys
				425					430					435
Gly	Cys	Gln	Ser	Leu	Pro	Ser	Asn	Met	Met	Glu	Thr	Ser	Ile	Asp
				440					445					450
Glu	Gly	Leu	Glu	Thr	Glu	Gly	Glu	Ala	Glu	Glu	Asp	Pro	Ala	His
				455					460					465
Ala	Phe	Glu	Ala	Phe	Gln	Ser	Thr	Arg	Ser	Gly	Gln	Arg	Arg	His
				470					475					480
Thr	Leu	Ser	Glu	Val	Thr	Asn	Gln	Leu	Val	Val	Met	Pro	Gly	Ala
				485					490					495
Gly	Lys	Ile	Phe	Ser	Met	Asn	Asp	Ser	Pro	Ser	Leu	Asp	Ser	Val
				500					505					510
Asp	Ser	Glu	Tyr	Asp	Met	Gly	Ser	Val	Gln	Arg	Asp	Leu	Asn	Phe
				515					520					525
Leu	Glu	Asp	Asn	Pro	Ser	Leu	Lys	Asp	Ile	Met	Leu	Ala	Asn	Gln
				530					535					540
Pro	Ser	Pro	Arg	Met	Thr	Ser	Pro	Phe	Ile	Ser	Leu	Arg	Pro	Thr
				545					550					555
Asn	Pro	Ala	Met	Gln	Ala	Leu	Ser	Ser	Gln	Lys	Arg	Glu	Val	His
				560					565					570
Asn	Arg	Ser	Pro	Val	Ser	Phe	Arg	Glu	Gly	Arg	Arg	Ala	Ser	Asp
				575					580					585
Thr	Ser	Leu	Thr	Gln	Gly	Ile	Val	Ala	Phe	Arg	Gln	His	Leu	Gln
				590					595					600
Asn	Leu	Ala	Arg	Thr	Lys	Gly	Ile	Leu	Glu	Leu	Asn	Lys	Val	Gln
				605					610					615
Leu	Leu	Tyr	Glu	Gln	Ile	Gly	Pro	Glu	Ala	Asp	Pro	Asn	Leu	Ala
				620					625					630
Pro	Ala	Ala	Pro	Gln	Leu	Gln	Asp	Leu	Ala	Ser	Ser	Cys	Pro	Gln
				635					640					645
Glu	Glu	Val	Ser	Gln	Gln	Gln	Glu	Ser	Val	Ser	Thr	Leu	Pro	Ala
				650					655					660
Ser	Val	His	Pro	Gln	Leu	Ser	Pro	Arg	Gln	Ser	Leu	Glu	Thr	Gln
				665					670					675
Tyr	Leu	Gln	His	Arg	Leu	Gln	Lys	Pro	Ser	Leu	Leu	Ser	Lys	Ala
				680					685					690
Gln	Asn	Thr	Cys	Gln	Leu	Tyr	Cys	Lys	Glu	Pro	Pro	Arg	Ser	Leu
				695					700					705
Glu	Gln	Gln	Leu	Gln	Glu	His	Arg	Leu	Gln	Gln	Lys	Arg	Leu	Phe
				710					715					720
Leu	Gln	Lys	Gln	Ser	Gln	Leu	Gln	Ala	Tyr	Phe	Asn	Gln	Met	Gln
				725					730					735
Ile	Ala	Glu	Ser	Ser	Tyr	Pro	Gln	Pro	Ser	Gln	Gln	Leu	Pro	Leu
				740					745					750
Pro	Arg	Gln	Glu	Thr	Pro	Pro	Pro	Ser	Gln	Gln	Ala	Pro	Pro	Phe
				755					760					765
Ser	Leu	Thr	Gln	Pro	Leu	Ser	Pro	Val	Leu	Glu	Pro	Ser	Ser	Glu

	770		775		780
Gln Met Gln Tyr Ser Pro Phe Leu Ser Gln Tyr Gln Glu Met Gln					
	785		790		795
Leu Gln Pro Leu Pro Ser Thr Ser Gly Pro Arg Ala Ala Pro Pro					
	800		805		810
Leu Pro Thr Gln Leu Gln Gln Gln Gln Pro Pro Pro Pro Pro					
	815		820		825
Pro Pro Pro Pro Arg Gln Pro Gly Ala Ala Pro Ala Pro Leu Gln					
	830		835		840
Phe Ser Tyr Gln Thr Cys Glu Leu Pro Ser Ala Ala Ser Pro Ala					
	845		850		855
Pro Asp Tyr Pro Thr Pro Cys Gln Tyr Pro Val Asp Gly Ala Gln					
	860		865		870
Gln Ser Asp Leu Thr Gly Pro Asp Cys Pro Arg Ser Pro Gly Leu					
	875		880		885
Gln Glu Ala Pro Ser Ser Tyr Asp Pro Leu Ala Leu Ser Glu Leu					
	890		895		900
Pro Gly Leu Phe Asp Cys Glu Met Leu Asp Ala Val Asp Pro Gln					
	905		910		915
His Asn Gly Tyr Val Leu Val Asn					
	920				

<210> 8

<211> 442

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4357117CD1

<400> 8

Met Arg Ile Val Cys Leu Val Lys Asn Gln Gln Pro Leu Gly Ala		
1	5	10
Thr Ile Lys Arg His Glu Met Thr Gly Asp Ile Leu Val Ala Arg		
	20	25
Ile Ile His Gly Gly Leu Ala Glu Arg Ser Gly Leu Leu Tyr Ala		
	35	40
Gly Asp Lys Leu Val Glu Val Asn Gly Val Ser Val Glu Gly Leu		
	50	55
Asp Pro Glu Gln Val Ile His Ile Leu Ala Met Ser Arg Gly Thr		
	65	70
Ile Met Phe Lys Val Val Pro Val Ser Asp Pro Pro Val Asn Ser		
	80	85
Gln Gln Met Val Tyr Val Arg Ala Met Thr Glu Tyr Trp Pro Gln		
	95	100
Glu Asp Pro Asp Ile Pro Cys Met Asp Ala Gly Leu Pro Phe Gln		
	110	115
Lys Gly Asp Ile Leu Gln Ile Val Asp Gln Asn Asp Ala Leu Trp		
	125	130
Trp Gln Ala Arg Lys Ile Ser Asp Pro Ala Thr Cys Ala Gly Leu		
	140	145
Val Pro Ser Asn His Leu Leu Lys Arg Lys Gln Arg Glu Phe Trp		
	155	160
Trp Ser Gln Pro Tyr Gln Pro His Thr Cys Leu Lys Ser Thr Ser		
	170	175
Asp Lys Glu Glu Phe Val Gly Tyr Gly Gln Lys Phe Phe Ile Gly		
	185	190
Arg Phe Ser Pro Leu His Ala Ser Val Cys Cys Thr Gly Ser Cys		
	200	205
Tyr Ser Ala Val Gly Ala Pro Tyr Glu Glu Val Val Arg Tyr Gln		
	215	220
Arg Arg Pro Ser Asp Lys Tyr Arg Leu Ile Val Leu Ile Gly Pro		

	230		235		240
Ser Gly Val Gly	Val Asn Glu Leu Arg	Arg Gln Leu Ile Glu Phe			
	245		250		255
Asn Pro Ser His	Phe Gln Ser Ala Val	Pro His Thr Thr Arg Thr			
	260		265		270
Lys Lys Ser Tyr	Glu Met Asn Gly Arg	Glu Tyr His Tyr Val Ser			
	275		280		285
Lys Glu Thr Phe	Glu Asn Leu Ile Tyr	Ser His Arg Met Leu Glu			
	290		295		300
Tyr Gly Glu Tyr	Lys Gly His Leu Tyr	Gly Thr Ser Val Asp Ala			
	305		310		315
Val Gln Thr Val	Leu Val Glu Gly Lys	Ile Cys Val Met Asp Leu			
	320		325		330
Glu Pro Gln Asp	Ile Gln Gly Val Arg	Thr His Glu Leu Lys Pro			
	335		340		345
Tyr Val Ile Phe	Ile Lys Pro Ser Asn	Met Arg Cys Met Lys Gln			
	350		355		360
Ser Arg Lys Asn	Ala Lys Val Ile Thr	Asp Tyr Tyr Val Asp Met			
	365		370		375
Lys Phe Lys Asp	Glu Asp Leu Gln Glu	Met Glu Asn Leu Ala Gln			
	380		385		390
Arg Met Glu Thr	Gln Phe Gly Gln Phe	Phe Asp His Val Ile Val			
	395		400		405
Asn Asp Ser Leu	His Asp Ala Cys Ala	Gln Leu Leu Ser Ala Ile			
	410		415		420
Gln Lys Ala Gln	Glu Pro Gln Trp	Val Pro Ala Thr Trp Ile			
	425		430		435
Ser Ser Asp Thr	Glu Ser Gln				
	440				

<210> 9

<211> 1046

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 5511992CD1

<400> 9

Met Glu Pro Ser Arg	Ala Leu Leu Gly Cys	Leu Ala Ser Ala Ala
1	5	10 15
Ala Ala Ala Pro Pro	Gly Glu Asp Gly Ala	Gly Ala Gly Ala Glu
	20	25 30
Glu Glu Glu Glu Glu	Glu Glu Glu Ala Ala	Ala Ala Val Gly Pro
	35	40 45
Gly Glu Leu Gly Cys	Asp Ala Pro Leu Pro	Tyr Trp Thr Ala Val
	50	55 60
Phe Glu Tyr Glu Ala	Ala Gly Glu Asp Glu	Leu Thr Leu Arg Leu
	65	70 75
Gly Asp Val Val Glu	Val Leu Ser Lys Asp	Ser Gln Val Ser Gly
	80	85 90
Asp Glu Gly Trp Trp	Thr Gly Gln Leu Asn	Gln Arg Val Gly Ile
	95	100 105
Phe Pro Ser Asn Tyr	Val Thr Pro Arg Ser	Ala Phe Ser Ser Arg
	110	115 120
Cys Gln Pro Gly Gly	Glu Glu Glu Ile Asp	Phe Ala Glu Leu Thr
	125	130 135
Leu Glu Glu Ile Ile	Gly Ile Gly Gly Phe	Gly Lys Val Tyr Arg
	140	145 150
Ala Phe Trp Ile Gly	Asp Glu Val Ala Val	Lys Ala Ala Arg His
	155	160 165
Asp Pro Asp Glu Asp	Ile Ser Gln Thr Ile	Glu Asn Val Arg Gln

	170		175		180
Glu Ala Lys Leu	Phe Ala Met Leu Lys	His Pro Asn Ile Ile	Ala		
	185		190		195
Leu Arg Gly Val	Cys Leu Lys Glu Pro	Asn Leu Cys Leu Val	Met		
	200		205		210
Glu Phe Ala Arg	Gly Gly Pro Leu Asn	Arg Val Leu Ser Gly	Lys		
	215		220		225
Arg Ile Pro Pro	Asp Ile Leu Val Asn	Trp Ala Val Gln Ile	Ala		
	230		235		240
Arg Gly Met Asn	Tyr Leu Leu Asp Glu	Ala Ile Val Pro Ile	Ile		
	245		250		255
His Arg Asp Leu	Lys Ser Ser Asn Ile	Leu Ile Leu Gln Lys	Val		
	260		265		270
Glu Asn Gly Asp	Leu Ser Asn Lys Ile	Leu Lys Ile Thr Asp	Phe		
	275		280		285
Gly Leu Ala Arg	Glu Trp His Arg Thr	Thr Lys Met Ser Ala	Ala		
	290		295		300
Gly Thr Tyr Ala	Trp Met Ala Pro Glu	Val Ile Arg Ala Ser	Met		
	305		310		315
Phe Ser Lys Gly	Ser Asp Val Trp Ser	Tyr Gly Val Leu Leu	Trp		
	320		325		330
Glu Leu Leu Thr	Gly Glu Val Pro Phe	Arg Gly Ile Asp Gly	Leu		
	335		340		345
Ala Val Ala Tyr	Gly Val Ala Met Asn	Lys Leu Ala Leu Pro	Ile		
	350		355		360
Pro Ser Thr Cys	Pro Glu Pro Phe Ala	Lys Leu Met Glu Asp	Cys		
	365		370		375
Trp Asn Pro Asp	Pro His Ser Arg Pro	Ser Phe Thr Asn Ile	Leu		
	380		385		390
Asp Gln Leu Thr	Thr Ile Glu Glu Ser	Gly Phe Phe Glu Met	Pro		
	395		400		405
Lys Asp Ser Phe	His Cys Leu Gln Asp	Asn Trp Lys His Glu	Ile		
	410		415		420
Gln Glu Met Phe	Asp Gln Leu Arg Ala	Lys Glu Lys Glu Leu	Arg		
	425		430		435
Thr Trp Glu Glu	Glu Leu Thr Arg Ala	Ala Leu Gln Gln Lys	Asn		
	440		445		450
Gln Glu Glu Leu	Leu Arg Arg Arg Glu	Gln Glu Leu Ala Glu	Arg		
	455		460		465
Glu Ile Asp Ile	Leu Glu Arg Glu Leu	Asn Ile Ile Ile His	Gln		
	470		475		480
Leu Cys Gln Glu	Lys Pro Arg Val Lys	Lys Arg Lys Gly Lys	Phe		
	485		490		495
Arg Lys Ser Arg	Leu Lys Leu Lys Asp	Gly Asn Arg Ile Ser	Leu		
	500		505		510
Pro Ser Gly Phe	Gln His Lys Phe Thr	Val Gln Ala Ser Pro	Thr		
	515		520		525
Met Asp Lys Arg	Lys Ser Leu Ile Asn	Ser Arg Ser Ser Pro	Pro		
	530		535		540
Ala Ser Pro Thr	Ile Ile Pro Arg Leu	Arg Ala Ile Gln Cys	Glu		
	545		550		555
Thr Val Ser Lys	Thr Trp Gly Arg Ser	Ser Val Val Pro Lys	Glu		
	560		565		570
Glu Gly Glu Glu	Glu Glu Lys Arg Ala	Pro Lys Lys Lys Gly	Arg		
	575		580		585
Thr Trp Gly Pro	Gly Thr Leu Gly Gln	Lys Glu Leu Ala Ser	Gly		
	590		595		600
Asp Glu Ser Leu	Lys Ser Leu Val Asp	Gly Tyr Lys Gln Trp	Ser		
	605		610		615
Ser Ser Ala Pro	Asn Leu Val Lys Gly	Pro Arg Ser Ser Pro	Ala		
	620		625		630
Leu Pro Gly Phe	Thr Ser Leu Met Glu	Met Gly Lys Phe Thr	Glu		
	635		640		645

Asp	Glu	Asp	Ser	Glu	Gly	Pro	Gly	Ser	Gly	Glu	Ser	Arg	Leu	Gln	
				650					655					660	
His	Ser	Pro	Ser	Gln	Ser	Tyr	Leu	Cys	Ile	Pro	Phe	Pro	Arg	Gly	
				665					670					675	
Glu	Asp	Gly	Asp	Gly	Pro	Ser	Ser	Asp	Gly	Ile	His	Glu	Glu	Pro	
				680					685					690	
Thr	Pro	Val	Asn	Ser	Ala	Thr	Ser	Thr	Pro	Gln	Leu	Thr	Pro	Thr	
				695					700					705	
Asn	Ser	Leu	Lys	Arg	Gly	Gly	Ala	His	His	Arg	Arg	Cys	Glu	Val	
				710					715					720	
Ala	Leu	Leu	Gly	Cys	Gly	Ala	Val	Leu	Ala	Ala	Thr	Gly	Leu	Gly	
				725					730					735	
Phe	Asp	Leu	Leu	Glu	Ala	Gly	Lys	Cys	Gln	Leu	Leu	Pro	Leu	Glu	
				740					745					750	
Glu	Pro	Glu	Pro	Pro	Ala	Arg	Glu	Glu	Lys	Lys	Arg	Arg	Glu	Gly	
				755					760					765	
Leu	Phe	Gln	Arg	Ser	Ser	Arg	Pro	Arg	Arg	Ser	Thr	Ser	Pro	Pro	
				770					775					780	
Ser	Arg	Lys	Leu	Phe	Lys	Lys	Glu	Glu	Pro	Met	Leu	Leu	Leu	Gly	
				785					790					795	
Asp	Pro	Ser	Ala	Ser	Leu	Thr	Leu	Leu	Ser	Leu	Ser	Ser	Ile	Ser	
				800					805					810	
Glu	Cys	Asn	Ser	Thr	Arg	Ser	Leu	Leu	Arg	Ser	Asp	Ser	Asp	Glu	
				815					820					825	
Ile	Val	Val	Tyr	Glu	Met	Pro	Val	Ser	Pro	Val	Glu	Ala	Pro	Pro	
				830					835					840	
Leu	Ser	Pro	Cys	Thr	His	Asn	Pro	Leu	Val	Asn	Val	Arg	Val	Glu	
				845					850					855	
Arg	Phe	Lys	Arg	Asp	Pro	Asn	Gln	Ser	Leu	Thr	Pro	Thr	His	Val	
				860					865					870	
Thr	Leu	Thr	Thr	Pro	Ser	Gln	Pro	Ser	Ser	His	Arg	Arg	Thr	Pro	
				875					880					885	
Ser	Asp	Gly	Ala	Leu	Pro	Ser	Pro	Ser	Arg	Asp	Pro	Gly	Glu	Phe	
				890					895					900	
Pro	Arg	Leu	Pro	Asp	Pro	Asn	Val	Val	Phe	Pro	Pro	Thr	Pro	Arg	
				905					910					915	
Arg	Trp	Asn	Thr	Gln	Gln	Asp	Ser	Thr	Leu	Glu	Arg	Pro	Lys	Thr	
				920					925					930	
Leu	Glu	Phe	Leu	Pro	Arg	Pro	Arg	Pro	Ser	Ala	Asn	Arg	Gln	Arg	
				935					940					945	
Leu	Asp	Pro	Trp	Trp	Phe	Val	Ser	Pro	Ser	His	Ala	Arg	Ser	Thr	
				950					955					960	
Ser	Pro	Ala	Asn	Ser	Ser	Ser	Thr	Glu	Thr	Pro	Ser	Asn	Leu	Asp	
				965					970					975	
Ser	Cys	Phe	Ala	Ser	Ser	Ser	Ser	Thr	Val	Glu	Glu	Arg	Pro	Gly	
				980					985					990	
Leu	Pro	Ala	Leu	Leu	Pro	Phe	Gln	Ala	Gly	Pro	Leu	Pro	Pro	Thr	
				995					1000					1005	
Glu	Arg	Thr	Leu	Leu	Asp	Leu	Asp	Ala	Glu	Gly	Gln	Ser	Gln	Asp	
				1010					1015					1020	
Ser	Thr	Val	Pro	Leu	Cys	Arg	Ala	Glu	Leu	Asn	Thr	His	Arg	Pro	
				1025					1030					1035	
Ala	Pro	Tyr	Glu	Ile	Gln	Gln	Glu	Phe	Trp	Ser					
				1040					1045						

<210> 10

<211> 357

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474560CD1

<400> 10
 Met Gln Ile Pro Asp Glu Glu Gly Ile Val Ile Asp Gly Phe Pro
 1 5 10 15
 Arg Asp Val Ala Gln Ala Leu Ser Phe Glu Asp Gln Ile Cys Thr
 20 25 30
 Pro Asp Leu Val Val Phe Leu Ala Cys Ala Asn Gln Arg Leu Lys
 35 40 45
 Glu Arg Leu Leu Lys Arg Ala Glu Gln Gln Gly Arg Pro Asp Asp
 50 55 60
 Asn Val Lys Ala Thr Gln Arg Arg Leu Met Asn Phe Lys Gln Asn
 65 70 75
 Ala Ala Pro Leu Val Lys Tyr Phe Gln Glu Lys Gly Leu Ile Met
 80 85 90
 Thr Phe Asp Ala Asp Arg Asp Glu Asp Glu Val Phe Tyr Asp Ile
 95 100 105
 Ser Met Ala Val Asp Asn Lys Leu Phe Pro Asn Lys Glu Ala Ala
 110 115 120
 Ala Gly Ser Ser Asp Leu Asp Pro Ser Met Ile Leu Asp Thr Gly
 125 130 135
 Glu Ile Ile Asp Thr Gly Ser Asp Tyr Glu Asp Gln Gly Asp Asp
 140 145 150
 Gln Leu Asn Val Phe Gly Glu Asp Thr Met Gly Gly Phe Met Glu
 155 160 165
 Asp Leu Arg Lys Cys Lys Ile Ile Phe Ile Ile Gly Gly Pro Gly
 170 175 180
 Ser Gly Lys Gly Thr Gln Cys Glu Lys Leu Val Glu Lys Tyr Gly
 185 190 195
 Phe Thr His Leu Ser Thr Gly Glu Leu Leu Arg Glu Glu Leu Ala
 200 205 210
 Ser Glu Ser Glu Arg Ser Lys Leu Ile Arg Asp Ile Met Glu Arg
 215 220 225
 Gly Asp Leu Val Pro Ser Gly Ile Val Leu Glu Leu Leu Lys Glu
 230 235 240
 Ala Met Val Ala Ser Leu Gly Asp Thr Arg Gly Phe Leu Ile Asp
 245 250 255
 Gly Tyr Pro Arg Glu Val Lys Gln Gly Glu Glu Phe Gly Arg Arg
 260 265 270
 Ile Gly Asp Pro Gln Leu Val Ile Cys Met Asp Cys Ser Ala Asp
 275 280 285
 Thr Met Thr Asn Arg Leu Leu Gln Arg Ser Arg Ser Ser Leu Pro
 290 295 300
 Val Asp Asp Thr Thr Lys Thr Ile Ala Lys Arg Leu Glu Ala Tyr
 305 310 315
 Tyr Arg Ala Ser Ile Pro Val Ile Ala Tyr Tyr Glu Thr Lys Thr
 320 325 330
 Gln Leu His Lys Ile Asn Ala Glu Gly Thr Pro Glu Asp Val Phe
 335 340 345
 Leu Gln Leu Cys Thr Ala Ile Asp Ser Ile Ile Phe
 350 355

<210> 11
 <211> 355
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7474602CD1

<400> 11
 Met Ala Arg Glu Asn Gly Glu Ser Ser Ser Trp Lys Lys Gln
 1 5 10 15
 Ala Glu Asp Ile Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly

	20		25		30
Thr Gly Ala Phe	Ser Glu Val Val Leu	Ala Glu Glu Lys Ala Thr			
	35		40		45
Gly Lys Leu Phe	Ala Val Lys Cys Ile	Pro Lys Lys Ala Leu Lys			
	50		55		60
Gly Lys Glu Ser	Ser Ile Glu Asn Glu	Ile Ala Val Leu Arg Lys			
	65		70		75
Ile Lys His Glu	Asn Ile Val Ala Leu	Glu Asp Ile Tyr Glu Ser			
	80		85		90
Pro Asn His Leu	Tyr Leu Val Met Gln	Leu Val Ser Gly Gly Glu			
	95		100		105
Leu Phe Asp Arg	Ile Val Glu Lys Gly	Phe Tyr Thr Glu Lys Asp			
	110		115		120
Ala Ser Thr Leu	Ile Arg Gln Val Leu	Asp Ala Val Tyr Tyr Leu			
	125		130		135
His Arg Met Gly	Ile Val His Arg Asp	Leu Lys Pro Glu Asn Leu			
	140		145		150
Leu Tyr Tyr Ser	Gln Asp Glu Glu Ser	Lys Ile Met Ile Ser Asp			
	155		160		165
Phe Gly Leu Ser	Lys Met Glu Gly Lys	Gly Asp Val Met Ser Thr			
	170		175		180
Ala Cys Gly Thr	Pro Gly Tyr Val Ala	Pro Glu Val Leu Ala Gln			
	185		190		195
Lys Pro Tyr Ser	Lys Ala Val Asp Cys	Trp Ser Ile Gly Val Ile			
	200		205		210
Ala Tyr Ile Leu	Leu Cys Gly Tyr Pro	Pro Phe Tyr Asp Glu Asn			
	215		220		225
Asp Ser Lys Leu	Phe Glu Gln Ile Leu	Lys Ala Glu Tyr Glu Phe			
	230		235		240
Asp Ser Pro Tyr	Trp Asp Asp Ile Ser	Asp Ser Ala Lys Asp Phe			
	245		250		255
Ile Arg Asn Leu	Met Glu Lys Asp Pro	Asn Lys Arg Tyr Thr Cys			
	260		265		270
Glu Gln Ala Ala	Arg His Pro Trp Ile	Ala Gly Asp Thr Ala Leu			
	275		280		285
Asn Lys Asn Ile	His Glu Ser Val Ser	Ala Gln Ile Arg Lys Asn			
	290		295		300
Phe Ala Lys Ser	Lys Trp Arg Gln Ala	Phe Asn Ala Thr Ala Val			
	305		310		315
Val Arg His Met	Arg Lys Leu His Leu	Gly Ser Ser Leu Asp Ser			
	320		325		330
Ser Asn Ala Ser	Val Ser Ser Ser Leu	Ser Leu Ala Ser Gln Lys			
	335		340		345
Asp Cys Ala Ser	Gly Thr Phe His Ala Leu				
	350		355		

<210> 12

<211> 224

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475509CD1

<400> 12

Met Ala Ser Lys Leu	Leu Arg Ala Val	Ile Leu Gly Pro Pro Gly
1	5	10 15
Ser Gly Lys Gly Thr	Val Cys Gln Arg	Ile Ala Gln Asn Phe Gly
	20	25 30
Leu Gln His Leu Ser	Ser Gly His Phe	Leu Arg Glu Asn Ile Lys
	35	40 45
Ala Ser Thr Glu Val	Gly Glu Met Ala	Lys Gln Tyr Ile Glu Lys

	50		55		60
Ser Leu Leu Val	Pro Asp His Val Ile Thr Arg Leu Met Met Ser				
	65		70		75
Glu Leu Glu Asn Arg Arg Gly Gln His Trp Leu Leu Asp Gly Phe					
	80		85		90
Pro Arg Thr Leu Gly Gln Ala Glu Ala Leu Asp Lys Ile Cys Glu					
	95		100		105
Val Asp Leu Val Ile Ser Leu Asn Ile Pro Phe Glu Thr Leu Lys					
	110		115		120
Asp Arg Leu Ser Arg Arg Trp Ile His Pro Pro Ser Gly Arg Val					
	125		130		135
Tyr Asn Leu Asp Phe Asn Pro Pro His Val His Gly Ile Asp Asp					
	140		145		150
Val Thr Gly Glu Pro Leu Val Gln Gln Glu Asp Asp Lys Pro Glu					
	155		160		165
Ala Val Ala Ala Arg Leu Arg Gln Tyr Lys Asp Val Ala Lys Pro					
	170		175		180
Val Ile Glu Leu Tyr Lys Ser Arg Gly Val Leu His Gln Phe Phe					
	185		190		195
Arg Asn Arg Arg Arg Thr Lys Ile Trp Pro Tyr Val Tyr Thr Thr					
	200		205		210
Phe Leu Asn Lys Ile Thr Pro Ile Gln Ser Lys Glu Ala Phe					
	215		220		

<210> 13

<211> 502

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475491CD1

<400> 13

Met Asn Lys Met Lys Asn Phe Lys Arg Arg Phe Ser Leu Ser Val		
1	5	10
Pro Arg Thr Glu Thr Ile Glu Glu Ser Leu Ala Glu Phe Thr Glu		
	20	25
Gln Phe Asn Gln Leu His Asn Arg Arg Asn Glu Asn Leu Gln Leu		
	35	40
Gly Pro Leu Gly Arg Asp Pro Pro Gln Glu Cys Ser Thr Phe Ser		
	50	55
Pro Thr Asp Ser Gly Glu Glu Pro Gly Gln Leu Ser Pro Gly Val		
	65	70
Gln Phe Gln Arg Arg Gln Asn Gln Arg Arg Phe Ser Met Glu Val		
	80	85
Arg Ala Ser Gly Ala Leu Pro Arg Gln Val Ala Gly Cys Thr His		
	95	100
Lys Gly Val His Arg Arg Ala Ala Ala Leu Gln Pro Asp Phe Asp		
	110	115
Val Ser Lys Arg Leu Ser Leu Pro Met Asp Ile Arg Leu Pro Gln		
	125	130
Glu Phe Leu Gln Lys Leu Gln Met Glu Ser Pro Asp Leu Pro Lys		
	140	145
Pro Leu Ser Arg Met Ser Arg Arg Ala Ser Leu Ser Asp Ile Gly		
	155	160
Phe Gly Lys Leu Glu Thr Tyr Val Lys Leu Asp Lys Leu Gly Glu		
	170	175
Gly Thr Tyr Ala Thr Val Phe Lys Gly Arg Ser Lys Leu Thr Glu		
	185	190
Asn Leu Val Ala Leu Lys Glu Ile Arg Leu Glu His Glu Glu Gly		
	200	205
Ala Pro Cys Thr Ala Ile Arg Glu Val Ser Leu Leu Lys Asn Leu		

	215		220		225
Lys His Ala Asn	Ile Val Thr Leu His	Asp Leu Ile His Thr	Asp		
	230		235		240
Arg Ser Leu Thr	Leu Val Phe Glu Tyr	Leu Asp Ser Asp Leu	Lys		
	245		250		255
Gln Tyr Leu Asp	His Cys Gly Asn Leu	Met Ser Met His Asn	Val		
	260		265		270
Lys Ile Phe Met	Phe Gln Leu Leu Arg	Gly Leu Ala Tyr Cys	His		
	275		280		285
His Arg Lys Ile	Leu His Arg Asp Leu	Lys Pro Gln Asn Leu	Leu		
	290		295		300
Ile Asn Glu Arg	Gly Glu Leu Lys Leu	Ala Asp Phe Gly Leu	Ala		
	305		310		315
Arg Ala Lys Ser	Val Pro Thr Lys Thr	Tyr Ser Asn Glu Val	Val		
	320		325		330
Thr Leu Trp Tyr	Arg Pro Pro Asp Val	Leu Leu Gly Ser Thr	Glu		
	335		340		345
Tyr Ser Thr Pro	Ile Asp Met Trp Gly	Val Gly Cys Ile His	Tyr		
	350		355		360
Glu Met Ala Thr	Gly Arg Pro Leu Phe	Pro Gly Ser Thr Val	Lys		
	365		370		375
Glu Glu Leu His	Leu Ile Phe Arg Leu	Leu Gly Thr Pro Thr	Glu		
	380		385		390
Glu Thr Trp Pro	Gly Val Thr Ala Phe	Ser Glu Phe Arg Thr	Tyr		
	395		400		405
Ser Phe Pro Cys	Tyr Leu Pro Gln Pro	Leu Ile Asn His Ala	Pro		
	410		415		420
Arg Leu Asp Thr	Asp Gly Ile His Leu	Leu Ser Ser Leu Leu	Leu		
	425		430		435
Tyr Glu Ser Lys	Ser Arg Met Ser Ala	Glu Ala Ala Leu Ser	His		
	440		445		450
Ser Tyr Phe Arg	Ser Leu Gly Glu Arg	Val His Gln Leu Glu	Asp		
	455		460		465
Thr Ala Ser Ile	Phe Ser Leu Lys Glu	Ile Gln Leu Gln Lys	Asp		
	470		475		480
Pro Gly Tyr Arg	Gly Leu Ala Phe Gln	Gln Pro Gly Arg Gly	Lys		
	485		490		495
Asn Arg Arg Gln	Ser Ile Phe				
	500				

<210> 14

<211> 791

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2192119CD1

<400> 14

Met Trp Phe Phe Ala	Arg Asp Pro Val Arg	Asp Phe Pro Phe Glu
1	5	10
Leu Ile Pro Glu Pro	Pro Glu Gly Gly Leu	Pro Gly Pro Trp Ala
	20	25
Leu His Arg Gly Arg	Lys Lys Ala Thr Gly	Ser Pro Val Ser Ile
	35	40
Phe Val Tyr Asp Val	Lys Pro Gly Ala Glu	Gln Thr Gln Val
	50	55
Ala Lys Ala Ala Phe	Lys Arg Phe Lys Thr	Leu Arg His Pro Asn
	65	70
Ile Leu Ala Tyr Ile	Asp Gly Leu Glu Thr	Glu Lys Cys Leu His
	80	85
Val Val Thr Glu Ala	Val Thr Pro Leu Gly	Ile Tyr Leu Lys Ala

	95		100		105
Arg Val Glu Ala	Gly Gly Leu Lys Glu	Leu Glu Ile Ser Trp	Gly		
	110		115		120
Leu His Gln Ile	Val Lys Ala Leu Ser	Phe Leu Val Asn Asp	Cys		
	125		130		135
Ser Leu Ile His	Asn Asn Val Cys Met	Ala Ala Val Phe Val	Asp		
	140		145		150
Arg Ala Gly Glu	Trp Lys Leu Gly Gly	Leu Asp Tyr Met Tyr	Ser		
	155		160		165
Ala Gln Gly Asn	Gly Gly Gly Pro Pro	Arg Lys Gly Ile Pro	Glu		
	170		175		180
Leu Glu Gln Tyr	Asp Pro Pro Glu Leu	Ala Asp Ser Ser Gly	Arg		
	185		190		195
Val Val Arg Glu	Lys Trp Ser Ala Asp	Met Trp Arg Leu Gly	Cys		
	200		205		210
Leu Ile Trp Glu	Val Phe Asn Gly Pro	Leu Pro Arg Ala Ala	Ala		
	215		220		225
Leu Arg Asn Pro	Gly Lys Ile Pro Lys	Thr Leu Val Pro His	Tyr		
	230		235		240
Cys Glu Leu Val	Gly Ala Asn Pro Lys	Val Arg Pro Asn Pro	Ala		
	245		250		255
Arg Phe Leu Gln	Asn Cys Arg Ala Pro	Gly Gly Phe Met Ser	Asn		
	260		265		270
Arg Phe Val Glu	Thr Asn Leu Phe Leu	Glu Glu Ile Gln Ile	Lys		
	275		280		285
Glu Pro Ala Glu	Lys Gln Lys Phe Phe	Gln Glu Leu Ser Lys	Ser		
	290		295		300
Leu Asp Ala Phe	Pro Glu Asp Phe Cys	Arg His Lys Val Leu	Pro		
	305		310		315
Gln Leu Leu Thr	Ala Phe Glu Phe Gly	Asn Ala Gly Ala Val	Val		
	320		325		330
Leu Thr Pro Leu	Phe Lys Val Gly Lys	Phe Leu Ser Ala Glu	Glu		
	335		340		345
Tyr Gln Gln Lys	Ile Ile Pro Val Val	Val Lys Met Phe Ser	Ser		
	350		355		360
Thr Asp Arg Ala	Met Arg Ile Arg Leu	Leu Gln Gln Met Glu	Gln		
	365		370		375
Phe Ile Gln Tyr	Leu Asp Glu Pro Thr	Val Asn Thr Gln Ile	Phe		
	380		385		390
Pro His Val Val	His Gly Phe Leu Asp	Thr Asn Pro Ala Ile	Arg		
	395		400		405
Glu Gln Thr Val	Lys Ser Met Leu Leu	Leu Ala Pro Lys Leu	Asn		
	410		415		420
Glu Ala Asn Leu	Asn Val Glu Leu Met	Lys His Phe Ala Arg	Leu		
	425		430		435
Gln Ala Lys Asp	Glu Gln Gly Pro Ile	Arg Cys Asn Thr Thr	Val		
	440		445		450
Cys Leu Gly Lys	Ile Gly Ser Tyr Leu	Ser Ala Ser Thr Arg	His		
	455		460		465
Arg Val Leu Thr	Ser Ala Phe Ser Arg	Ala Thr Arg Asp Pro	Phe		
	470		475		480
Ala Pro Ser Arg	Val Ala Gly Val Leu	Gly Phe Ala Ala Thr	His		
	485		490		495
Asn Leu Tyr Ser	Met Asn Asp Cys Ala	Gln Lys Ile Leu Pro	Val		
	500		505		510
Leu Cys Gly Leu	Thr Val Asp Pro Glu	Lys Ser Val Arg Asp	Gln		
	515		520		525
Ala Phe Lys Ala	Ile Arg Ser Phe Leu	Ser Lys Leu Glu Ser	Val		
	530		535		540
Ser Glu Asp Pro	Thr Gln Leu Glu Glu	Val Glu Lys Asp Val	His		
	545		550		555
Ala Ala Ser Ser	Pro Gly Met Gly Gly	Ala Ala Ser Trp	Ala		
	560		565		570

Gly Trp Ala Val	Thr Gly Val Ser Ser	Leu Thr Ser Lys Leu Ile
575	580	585
Arg Ser His Pro	Thr Thr Ala Pro Thr	Glu Thr Asn Ile Pro Gln
590	595	600
Arg Pro Thr Pro	Glu Gly His Trp Glu	Thr Gln Glu Glu Asp Lys
605	610	615
Asp Thr Ala Glu	Asp Ser Ser Thr Ala	Asp Arg Trp Asp Asp Glu
620	625	630
Asp Trp Gly Ser	Leu Glu Gln Glu Ala	Glu Ser Val Leu Ala Gln
635	640	645
Gln Asp Asp Trp	Ser Thr Gly Gly Gln	Val Ser Arg Ala Ser Gln
650	655	660
Val Ser Asn Ser	Asp His Lys Ser Ser	Lys Ser Pro Glu Ser Asp
665	670	675
Trp Ser Ser Trp	Glu Ala Glu Gly Ser	Trp Glu Gln Gly Trp Gln
680	685	690
Glu Pro Ser Ser	Gln Glu Pro Pro Pro	Asp Gly Thr Arg Leu Ala
695	700	705
Ser Glu Tyr Asn	Trp Gly Gly Pro Glu	Ser Ser Asp Lys Gly Asp
710	715	720
Pro Phe Ala Thr	Leu Ser Ala Arg Pro	Ser Thr Gln Pro Arg Pro
725	730	735
Asp Ser Trp Gly	Glu Asp Asn Trp Glu	Gly Leu Glu Thr Asp Ser
740	745	750
Arg Gln Val Lys	Ala Glu Leu Ala Arg	Lys Lys Arg Glu Glu Arg
755	760	765
Arg Arg Glu Met	Glu Ala Lys Arg Ala	Glu Arg Lys Val Ala Lys
770	775	780
Gly Pro Met Lys	Leu Gly Ala Arg Lys	Leu Asp
785	790	

<210> 15

<211> 1651

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7474496CD1

<400> 15

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Pro Glu Ser Tyr Pro	Gln Arg Gln Asp His	Glu Leu Gln Ala Leu
20	25	30
Glu Ala Ile Tyr Gly	Ala Asp Phe Gln Asp	Leu Arg Pro Asp Ala
35	40	45
Cys Gly Pro Val Lys	Glu Pro Pro Glu Ile	Asn Leu Val Leu Tyr
50	55	60
Pro Gln Gly Leu Thr	Gly Glu Glu Val Tyr	Val Lys Val Asp Leu
65	70	75
Arg Val Lys Cys Pro	Thr Tyr Pro Asp	Val Val Pro Glu Ile
80	85	90
Glu Leu Lys Asn Ala	Lys Gly Leu Ser Asn	Glu Ser Val Asn Leu
95	100	105
Leu Lys Ser Arg Leu	Glu Glu Leu Ala Lys	Lys His Cys Gly Glu
110	115	120
Val Met Ile Phe Glu	Leu Ala Tyr His Val	Gln Ser Phe Leu Ser
125	130	135
Glu His Asn Lys Pro	Pro Pro Lys Ser Phe	His Glu Glu Met Leu
140	145	150
Glu Arg Arg Ala Gln	Glu Glu Gln Gln Arg	Leu Leu Glu Ala Gln
155	160	165

Ala Glu Arg Arg	Arg Glu Gln Ala Gln	Gln Arg Glu Ile Leu His	170	175	180
Glu Ile Gln Arg	Arg Lys Glu Glu Ile	Lys Glu Glu Lys Lys Arg	185	190	195
Lys Glu Met Ala	Lys Gln Glu Arg Leu	Glu Ile Ala Ser Leu Ser	200	205	210
Asn Gln Asp His	Thr Ser Lys Lys Asp	Pro Gly Gly His Arg Thr	215	220	225
Ala Ala Ile Leu	His Gly Gly Ser Pro	Asp Phe Val Gly Asn Gly	230	235	240
Lys His Arg Ala	Asn Ser Ser Gly Arg	Ser Arg Arg Glu Arg Gln	245	250	255
Tyr Ser Val Cys	Asn Ser Glu Asp Ser	Pro Gly Ser Cys Glu Ile	260	265	270
Leu Tyr Phe Asn	Met Gly Ser Pro Asp	Gln Leu Met Val His Lys	275	280	285
Gly Lys Cys Ile	Gly Ser Asp Glu Gln	Leu Gly Lys Leu Val Tyr	290	295	300
Asn Ala Leu Glu	Thr Ala Thr Gly Gly	Phe Val Leu Leu Tyr Glu	305	310	315
Trp Val Leu Gln	Trp Gln Lys Lys Met	Gly Pro Phe Leu Thr Ser	320	325	330
Gln Glu Lys Glu	Lys Ile Asp Lys Cys	Lys Lys Gln Ile Gln Gly	335	340	345
Thr Glu Thr Glu	Phe Asn Ser Leu Val	Lys Leu Ser His Pro Asn	350	355	360
Val Val Arg Tyr	Leu Ala Met Asn Leu	Lys Glu Gln Asp Asp Ser	365	370	375
Ile Val Val Asp	Ile Leu Val Glu His	Ile Ser Gly Val Ser Leu	380	385	390
Ala Ala His Leu	Ser His Ser Gly Pro	Ile Pro Val His Gln Leu	395	400	405
Arg Arg Tyr Thr	Ala Gln Leu Leu Ser	Gly Leu Asp Tyr Leu His	410	415	420
Ser Asn Ser Val	Val His Lys Val Leu	Ser Ala Ser Asn Val Leu	425	430	435
Val Asp Ala Glu	Gly Thr Val Lys Ile	Thr Asp Tyr Ser Ile Ser	440	445	450
Lys Arg Leu Ala	Asp Ile Cys Lys Glu	Asp Val Phe Glu Gln Thr	455	460	465
Arg Val Arg Phe	Ser Asp Asn Ala Leu	Pro Tyr Lys Thr Gly Lys	470	475	480
Lys Gly Asp Val	Trp Arg Leu Gly Leu	Leu Leu Leu Ser Leu Ser	485	490	495
Gln Gly Gln Glu	Cys Gly Glu Tyr Pro	Val Thr Ile Pro Ser Asp	500	505	510
Leu Pro Ala Asp	Phe Gln Asp Phe Leu	Lys Cys Val Cys Leu Asp	515	520	525
Asp Lys Glu Arg	Trp Ser Pro Gln Gln	Leu Leu Lys His Ser Phe	530	535	540
Ile Asn Pro Gln	Pro Lys Met Pro Leu	Val Glu Gln Ser Pro Glu	545	550	555
Asp Ser Glu Gly	Gln Asp Tyr Val Glu	Thr Val Ile Pro Ser Asn	560	565	570
Arg Leu Pro Ser	Ala Ala Phe Phe Ser	Glu Thr Gln Arg Gln Phe	575	580	585
Ser Arg Tyr Phe	Ile Glu Phe Glu Glu	Leu Gln Leu Leu Gly Lys	590	595	600
Gly Ala Phe Gly	Ala Val Ile Lys Val	Gln Asn Lys Leu Asp Gly	605	610	615
Cys Cys Tyr Ala	Val Lys Arg Ile Pro	Ile Asn Pro Ala Ser Arg	620	625	630
Gln Phe Arg Arg	Ile Lys Gly Glu Val	Thr Leu Leu Ser Arg Leu			

His His Glu Asn	635	Ile Val Arg Tyr Tyr	640	Asn Ala Trp Ile Glu Arg	645
	650		655		660
His Glu Arg Pro	665	Ala Gly Pro Gly Thr	670	Pro Pro Pro Asp Ser Gly	675
Pro Leu Ala Lys	680	Asp Asp Arg Ala Ala	685	Arg Gly Gln Pro Ala Ser	690
Asp Thr Asp Gly	695	Leu Asp Ser Val Glu	700	Ala Ala Pro Pro Pro	705
Ile Leu Ser Ser	710	Ser Val Glu Trp Ser	715	Thr Ser Gly Glu Arg Ser	720
Ala Ser Ala Arg	725	Phe Pro Ala Thr Gly	730	Pro Gly Ser Ser Asp Asp	735
Glu Asp Asp Asp	740	Glu Asp Glu His Gly	745	Gly Val Phe Ser Gln Ser	750
Phe Leu Pro Ala	755	Ser Asp Ser Glu Ser	760	Asp Ile Ile Phe Asp Asn	765
Glu Asp Glu Asn	770	Ser Lys Ser Gln Asn	775	Gln Asp Glu Asp Cys Asn	780
Glu Lys Asn Gly	785	Cys His Glu Ser Glu	790	Pro Ser Val Thr Thr Glu	795
Ala Val His Tyr	800	Leu Tyr Ile Gln Met	805	Glu Tyr Cys Glu Lys Ser	810
Thr Leu Arg Asp	815	Thr Ile Asp Gln Gly	820	Leu Tyr Arg Asp Thr Val	825
Arg Leu Trp Arg	830	Leu Phe Arg Glu Ile	835	Leu Asp Gly Leu Ala Tyr	840
Ile His Glu Lys	845	Gly Met Ile His Arg	850	Asp Leu Lys Pro Val Asn	855
Ile Phe Leu Asp	860	Ser Asp Asp His Val	865	Lys Ile Gly Asp Phe Gly	870
Leu Ala Thr Asp	875	His Leu Ala Phe Ser	880	Ala Asp Ser Lys Gln Asp	885
Asp Gln Thr Gly	890	Asp Leu Ile Lys Ser	895	Asp Pro Ser Gly His Leu	900
Thr Gly Met Val	905	Gly Thr Ala Leu Tyr	910	Val Ser Pro Glu Val Gln	915
Gly Ser Thr Lys	920	Ser Ala Tyr Asn Gln	925	Lys Val Asp Leu Phe Ser	930
Leu Gly Ile Ile	935	Phe Phe Glu Met Ser	940	Tyr His Pro Met Val Thr	945
Ala Ser Glu Arg	950	Ile Phe Val Leu Asn	955	Gln Leu Arg Asp Pro Thr	960
Ser Pro Lys Phe	965	Pro Glu Asp Phe Asp	970	Asp Gly Glu His Ala Lys	975
Gln Lys Ser Val	980	Ile Ser Trp Leu Leu	985	Asn His Asp Pro Ala Lys	990
Arg Pro Thr Ala	995	Thr Glu Leu Leu Lys	1000	Ser Glu Leu Leu Pro Pro	1005
Pro Gln Met Glu	1010	Glu Ser Glu Leu His	1015	Glu Val Leu His His Thr	1020
Leu Thr Asn Val	1025	Asp Gly Lys Ala Tyr	1030	Arg Thr Met Met Ala Gln	1035
Ile Phe Ser Gln	1040	Arg Ile Ser Pro Ala	1045	Ile Asp Tyr Thr Tyr Asp	1050
Ser Asp Ile Leu	1055	Lys Gly Asn Phe Ser	1060	Ile Arg Thr Ala Lys Met	1065
Gln Gln His Val	1070	Cys Glu Thr Ile Ile	1075	Arg Ile Phe Lys Arg His	1080
Gly Ala Val Gln	1085	Leu Cys Thr Pro Leu	1090	Leu Leu Pro Arg Asn Arg	1095
Gln Ile Tyr Glu	1100	His Asn Glu Ala Ala	1105	Leu Phe Met Asp His Ser	1110

Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg Ile Pro Phe Ala
 1115 1120 1125
 Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr Cys
 1130 1135 1140
 Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His Pro
 1145 1150 1155
 Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr
 1160 1165 1170
 Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu
 1175 1180 1185
 Ile Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile
 1190 1195 1200
 Tyr Leu Asn His Thr Met Leu Leu Lys Ala Ile Leu Leu His Cys
 1205 1210 1215
 Gly Ile Pro Glu Asp Lys Leu Ser Gln Val Tyr Ile Ile Leu Tyr
 1220 1225 1230
 Asp Ala Val Thr Glu Lys Leu Thr Arg Arg Glu Val Glu Ala Lys
 1235 1240 1245
 Phe Cys Asn Leu Ser Leu Ser Ser Asn Ser Leu Cys Arg Leu Tyr
 1250 1255 1260
 Lys Phe Ile Glu Gln Lys Gly Asp Leu Gln Asp Leu Met Pro Thr
 1265 1270 1275
 Ile Asn Ser Leu Ile Lys Gln Lys Thr Gly Ile Ala Gln Leu Val
 1280 1285 1290
 Lys Tyr Gly Leu Lys Asp Leu Glu Glu Val Val Gly Leu Leu Lys
 1295 1300 1305
 Lys Leu Gly Ile Lys Leu Gln Val Leu Ile Asn Leu Gly Leu Val
 1310 1315 1320
 Tyr Lys Val Gln Gln His Asn Gly Ile Ile Phe Gln Phe Val Ala
 1325 1330 1335
 Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu Ile Leu Ala Ala
 1340 1345 1350
 Gly Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg Gly Pro Gln
 1355 1360 1365
 Ala Leu Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile Ala Ile
 1370 1375 1380
 Asp Lys Ile Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val Thr
 1385 1390 1395
 Ile Ser Ser Cys Asp Leu Leu Val Val Ser Val Gly Gln Met Ser
 1400 1405 1410
 Met Ser Arg Ala Ile Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly
 1415 1420 1425
 Ile Thr Ala Glu Ile Met Tyr Asp Trp Ser Gln Ser Gln Glu Glu
 1430 1435 1440
 Leu Gln Glu Tyr Cys Arg His His Glu Ile Thr Tyr Val Ala Leu
 1445 1450 1455
 Val Ser Asp Lys Glu Gly Ser His Val Lys Val Lys Ser Phe Glu
 1460 1465 1470
 Lys Glu Arg Gln Thr Glu Lys Arg Val Leu Glu Thr Glu Leu Val
 1475 1480 1485
 Asp His Val Leu Gln Lys Leu Arg Thr Lys Val Thr Asp Glu Arg
 1490 1495 1500
 Asn Gly Arg Glu Ala Ser Asp Asn Leu Ala Val Gln Asn Leu Lys
 1505 1510 1515
 Gly Ser Phe Ser Asn Ala Ser Gly Leu Phe Glu Ile His Gly Ala
 1520 1525 1530
 Thr Val Val Pro Ile Val Ser Val Leu Ala Pro Glu Lys Leu Ser
 1535 1540 1545
 Ala Ser Thr Arg Arg Arg Tyr Glu Thr Gln Val Gln Thr Arg Leu
 1550 1555 1560
 Gln Thr Ser Leu Ala Asn Leu His Gln Lys Ser Ser Glu Ile Glu
 1565 1570 1575
 Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu Gln Phe Leu

1580	1585	1590
Ser Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr Thr Val		
1595	1600	1605
Lys Gln Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys Leu		
1610	1615	1620
Val Cys Asp Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser		
1625	1630	1635
Val Leu Phe Leu Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu		
1640	1645	1650
Phe		

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 <211> 752
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 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 1834248CD1

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	20	25
Pro Ser Trp Ser Ser Arg Ser Leu Gly Ala Arg Cys Arg Asn Ser		
	35	40
Ile Ala Ser Cys Pro Glu Glu Gln Pro His Val Gly Asn Tyr Arg		
	50	55
Leu Leu Arg Thr Ile Gly Lys Gly Asn Phe Ala Lys Val Lys Leu		
	65	70
Ala Arg His Ile Leu Thr Gly Arg Glu Val Ala Ile Lys Ile Ile		
	80	85
Asp Lys Thr Gln Leu Asn Pro Ser Ser Leu Gln Lys Leu Phe Arg		
	95	100
Glu Val Arg Ile Met Lys Gly Leu Asn His Pro Asn Ile Val Lys		
	110	115
Leu Phe Glu Val Ile Glu Thr Glu Lys Thr Leu Tyr Leu Val Met		
	125	130
Glu Tyr Ala Ser Ala Gly Glu Val Phe Asp Tyr Leu Val Ser His		
	140	145
Gly Arg Met Lys Glu Lys Glu Ala Arg Ala Lys Phe Arg Gln Ile		
	155	160
Val Ser Ala Val His Tyr Cys His Gln Lys Asn Ile Val His Arg		
	170	175
Asp Leu Lys Ala Glu Asn Leu Leu Leu Asp Ala Glu Ala Asn Ile		
	185	190
Lys Ile Ala Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser		
	200	205
Lys Leu Asp Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu		
	215	220
Leu Phe Gln Gly Lys Lys Tyr Asp Gly Pro Glu Val Asp Ile Trp		
	230	235
Ser Leu Gly Val Ile Leu Tyr Thr Leu Val Ser Gly Ser Leu Pro		
	245	250
Phe Asp Gly His Asn Leu Lys Glu Leu Arg Glu Arg Val Leu Arg		
	260	265
Gly Lys Tyr Arg Val Pro Phe Tyr Met Ser Thr Asp Cys Glu Ser		
	275	280
Ile Leu Arg Arg Phe Leu Val Leu Asn Pro Ala Lys Arg Cys Thr		
	290	295
Leu Glu Gln Ile Met Lys Asp Lys Trp Ile Asn Ile Gly Tyr Glu		

	305		310		315
Gly Glu Glu Leu	Lys Pro Tyr Thr Glu	Pro Glu Glu Asp Phe	Gly		
	320		325		330
Asp Thr Lys Arg	Ile Glu Val Met Val	Gly Met Gly Tyr Thr	Arg		
	335		340		345
Glu Glu Ile Lys	Glu Ser Leu Thr Ser	Gln Lys Tyr Asn Glu	Val		
	350		355		360
Thr Ala Thr Tyr	Leu Leu Leu Gly Arg	Lys Thr Glu Glu Gly	Gly		
	365		370		375
Asp Arg Gly Ala	Pro Gly Leu Ala Leu	Ala Arg Val Arg Ala	Pro		
	380		385		390
Ser Asp Thr Thr	Asn Gly Thr Ser Ser	Ser Lys Gly Thr Ser	His		
	395		400		405
Ser Lys Gly Gln	Arg Ser Ser Ser Ser	Thr Tyr His Arg Gln	Arg		
	410		415		420
Arg His Ser Asp	Phe Cys Gly Pro Ser	Pro Ala Pro Leu His	Pro		
	425		430		435
Lys Arg Ser Pro	Thr Ser Thr Gly Glu	Ala Glu Leu Lys Glu	Glu		
	440		445		450
Arg Leu Pro Gly	Arg Lys Ala Ser Cys	Ser Thr Ala Gly Ser	Gly		
	455		460		465
Ser Arg Gly Leu	Pro Pro Ser Ser Pro	Met Val Ser Ser Ala	His		
	470		475		480
Asn Pro Asn Lys	Ala Glu Ile Pro Glu	Arg Arg Lys Asp Ser	Thr		
	485		490		495
Ser Thr Pro Asn	Asn Leu Pro Pro Ser	Met Met Thr Arg Arg	Asn		
	500		505		510
Thr Tyr Val Cys	Thr Glu Arg Pro Gly	Ala Glu Arg Pro Ser	Leu		
	515		520		525
Leu Pro Asn Gly	Lys Glu Asn Ser Ser	Gly Thr Pro Arg Val	Pro		
	530		535		540
Pro Ala Ser Pro	Ser Ser His Ser Leu	Ala Pro Pro Ser Gly	Glu		
	545		550		555
Arg Ser Arg Leu	Ala Arg Gly Ser Thr	Ile Arg Ser Thr Phe	His		
	560		565		570
Gly Gly Gln Val	Arg Asp Arg Arg Ala	Gly Gly Gly Gly Gly	Gly		
	575		580		585
Gly Val Gln Asn	Gly Pro Pro Ala Ser	Pro Thr Leu Ala His	Glu		
	590		595		600
Ala Ala Pro Leu	Pro Ala Gly Arg Pro	Arg Pro Thr Thr Asn	Leu		
	605		610		615
Phe Thr Lys Leu	Thr Ser Lys Leu Thr	Arg Arg Val Ala Asp	Glu		
	620		625		630
Pro Glu Arg Ile	Gly Gly Pro Glu Val	Thr Ser Cys His Leu	Pro		
	635		640		645
Trp Asp Gln Thr	Glu Thr Ala Pro Arg	Leu Leu Arg Phe Pro	Trp		
	650		655		660
Ser Val Lys Leu	Thr Ser Ser Arg Pro	Pro Glu Ala Leu Met	Ala		
	665		670		675
Ala Leu Arg Gln	Ala Thr Ala Ala Ala	Arg Cys Arg Cys Arg	Gln		
	680		685		690
Pro Gln Pro Phe	Leu Leu Ala Cys Leu	His Gly Gly Ala Gly	Gly		
	695		700		705
Pro Glu Pro Leu	Ser His Phe Glu Val	Glu Val Cys Gln Leu	Pro		
	710		715		720
Arg Pro Gly Leu	Arg Gly Val Leu Phe	Arg Arg Val Ala Gly	Thr		
	725		730		735
Ala Leu Ala Phe	Arg Thr Leu Val Thr	Arg Ile Ser Asn Asp	Leu		
	740		745		750
Glu Leu					

<210> 17

<211> 501
 <212> PRT
 <213> Homo sapiens

<220>
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 35 40 45
 Thr Gly Lys Leu His Thr Cys Lys Lys Phe Gln Lys Arg Asp Gly
 50 55 60
 Arg Lys Val Arg Lys Ala Ala Lys Asn Glu Ile Gly Ile Leu Lys
 65 70 75
 Met Val Lys His Pro Asn Ile Leu Gln Leu Val Asp Val Phe Val
 80 85 90
 Thr Arg Lys Glu Tyr Phe Ile Phe Leu Glu Leu Ala Thr Gly Arg
 95 100 105
 Glu Val Phe Asp Trp Ile Leu Asp Gln Gly Tyr Tyr Ser Glu Arg
 110 115 120
 Asp Thr Ser Asn Val Val Arg Gln Val Leu Glu Ala Val Ala Tyr
 125 130 135
 Leu His Ser Leu Lys Ile Val His Arg Asn Leu Lys Leu Glu Asn
 140 145 150
 Leu Val Tyr Tyr Asn Arg Leu Lys Asn Ser Lys Ile Val Ile Ser
 155 160 165
 Asp Phe His Leu Ala Lys Leu Glu Asn Gly Leu Ile Lys Glu Pro
 170 175 180
 Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Val Gly Arg Gln
 185 190 195
 Arg Tyr Gly Arg Pro Val Asp Cys Trp Ala Ile Gly Val Ile Met
 200 205 210
 Tyr Ile Leu Leu Ser Gly Asn Pro Pro Phe Tyr Glu Glu Val Glu
 215 220 225
 Glu Asp Asp Tyr Glu Asn His Asp Lys Asn Leu Phe Arg Lys Ile
 230 235 240
 Leu Ala Gly Asp Tyr Glu Phe Asp Ser Pro Tyr Trp Asp Asp Ile
 245 250 255
 Ser Gln Ala Ala Lys Asp Leu Val Thr Arg Leu Met Glu Val Glu
 260 265 270
 Gln Asp Gln Arg Ile Thr Ala Glu Glu Ala Ile Ser His Glu Trp
 275 280 285
 Ile Ser Gly Asn Ala Ala Ser Asp Lys Asn Ile Lys Asp Gly Val
 290 295 300
 Cys Ala Gln Ile Glu Lys Asn Phe Ala Arg Ala Lys Trp Lys Lys
 305 310 315
 Ala Val Arg Val Thr Thr Leu Met Lys Arg Leu Arg Ala Pro Glu
 320 325 330
 Gln Ser Ser Thr Ala Ala Ala Gln Ser Ala Ser Ala Thr Asp Thr
 335 340 345
 Ala Thr Pro Gly Ala Ala Gly Gly Ala Thr Ala Ala Ala Ala Ser
 350 355 360
 Gly Ala Thr Ser Ala Pro Glu Gly Asp Ala Ala Arg Ala Ala Lys
 365 370 375
 Ser Asp Asn Val Ala Pro Ala Asp Arg Ser Ala Thr Pro Ala Thr
 380 385 390
 Asp Gly Ser Ala Thr Pro Ala Thr Asp Gly Ser Val Thr Pro Ala
 395 400 405

Thr Asp Gly Ser Ile Thr Pro Ala Thr Asp Gly Ser Val Thr Pro	410	415	420
Ala Thr Asp Arg Ser Ala Thr Pro Ala Thr Asp Gly Arg Ala Thr	425	430	435
Pro Ala Thr Glu Glu Ser Thr Val Pro Thr Thr Gln Ser Ser Ala	440	445	450
Met Leu Ala Thr Lys Ala Ala Ala Thr Pro Glu Pro Ala Met Ala	455	460	465
Gln Pro Asp Ser Thr Ala Pro Glu Gly Ala Thr Gly Gln Ala Pro	470	475	480
Pro Ser Ser Lys Gly Glu Glu Ala Ala Gly Tyr Ala Gln Glu Ser	485	490	495
Gln Arg Glu Glu Ala Ser	500		

<210> 18

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7475538CD1

<400> 18

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Gly Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val	20	25	30	
Ala Leu Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro	35	40	45	
Asn Gln Ala Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp	50	55	60	
Asn Gln Tyr Val Val Gln Leu Lys Ala Val Phe Pro His Gly Gly	65	70	75	
Gly Phe Val Leu Ala Phe Glu Phe Met Leu Ser Asp Leu Ala Glu	80	85	90	
Val Val Arg His Ala Gln Arg Pro Leu Ala Gln Ala Gln Val Lys	95	100	105	
Ser Tyr Leu Gln Met Leu Leu Lys Gly Val Ala Phe Cys His Ala	110	115	120	
Asn Asn Ile Val His Arg Asp Leu Lys Pro Ala Asn Leu Leu Ile	125	130	135	
Ser Ala Ser Gly Gln Leu Lys Ile Ala Asp Phe Gly Leu Ala Arg	140	145	150	
Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr Thr His Gln Val Ala	155	160	165	
Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr Gly Ala Arg Gln	170	175	180	
Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys Ile Met Gly	185	190	195	
Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile	200	205	210	
Glu Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro	215	220	225	
Gln Val Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile	230	235	240	
Ser Phe Lys Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro	245	250	255	
Asp Val Ser Pro Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu	260	265	270	
Tyr Pro Pro His Gln Arg Ile Ala Ala Ser Lys Ala Leu Leu His	275	280	285	

Gln Tyr Phe Phe Thr Ala Pro Leu Pro Ala His Pro Ser Glu Leu
 290 295 300
 Pro Ile Pro Gln Arg Leu Gly Gly Pro Ala Pro Lys Ala His Pro
 305 310 315
 Gly Pro Pro His Ile His Asp Phe His Val Asp Arg Pro Leu Glu
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 Glu Ser Leu Leu Asn Pro Glu Leu Ile Arg Pro Phe Ile Leu Glu
 335 340 345
 Gly

<210> 19

<211> 4224

<212> DNA

<213> Homo sapiens

<220>

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<223> Incyte ID No: 2890544CB1

<400> 19

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<211> 1824

<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 3107952CB1

<400> 21

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<212> DNA

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<211> 2974

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<212> DNA

<213> Homo sapiens

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<223> Incyte ID No: 1834248CB1

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<213> Homo sapiens

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<223> Incyte ID No: 71584520CB1

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